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STIC-	-Biotech	n/ChemL	ib

From: Sent: To: Subject:

Chan, Christina

Thursday, January 24, 2002 2:49 PM Kemmerer, Elizabeth; STIC-Biotech/ChemLib

RE: rush seq search req

Hease rush. Thanks Chris

-----Original Message-----

From:

Kemmerer, Elizabeth

Sent:

Thursday, January 24, 2002 2:27 PM

To:

Chan, Christina

Subject:

rush seq search req

Hi Christina-

Please approve the following for a due amended:

STIC:

Please do a regular and interferences search of SEQ ID NO: 26 (full length) and an oligo search of 30 contiguous amino acids of SEQ ID NO: 26 for 08/741095

Thanks,

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17

Mailbox: 10C01

Searcher:
Phone:
Location:
Date Picked Up: 1941
Date Completed: ///25/107
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

Other:

VENDOR/COST(v	where applic.)
STN:	
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SHVEM1-FC fusion N
Hepatitis C virus
Hepatitis C virus
Immunogenic peptid
Cytotoxic T Lympho
Hepatitis C virus

New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening

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	BIOTHERAPEUTICS INC.						ry media human; autoimm	peptide.			10 AA.	ALIGNMENTS	AAJ01955 AAJ01956 AAR44066 AAR990379 AAW85437 AAW85437 AAJ73097 AAJ7003277 AAJ703277 AAJ00032	AAJ03940 AAB45928 AAB35060 AAJ01008	AAB62309 AAJ01007 AAJ01537 AAJ02965	AAY58923 AAY43814 AAG95144 AAU03164	AAY4644 AAY46516 AAB15407 AAY88069	AAJ03901 AAY49753 AAY46038	AAJ02614 AAJ03766
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							9-receptor; virus; therapy;						Hepatitis C virus Hepatitis C virus Pulmonary surfacta Sequence of antige Helper T-cell clas Human mIGE Cepsilo Hepatitis C virus	ဂရိုရိုဂ	Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus		nic I	patitis C virus mpact structure pepti	titis C vi titis C vi

assays

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Example

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                    The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                              Disclosure;
                                                                                                                                              WPI; 2001-308046/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminus of a mature human TANGO-69-receptor:IgG1 Fc fusion protein. The fusion protein was expressed in HEK 293T cells that had been transfected with a vector carrying a gene fusion composed of the human TANGO-69-receptor (sHVEMI, see AAZ94195) coding sequence and DNA encoding the Fc domain of human IgG1. sHVEMI (see also AAY9204) is a novel soluble form of membrane-bound herpesvirus entry
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Human leukocyte antigen; binding; immunogenic; glycoprotein; immune response; T cell activation; major histocompatibility
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                                                                     AAY47926;
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                             Immunogenic peptide having a human leukocyte antigen binding motif #2537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            having a human major histocompatibility complex (MHC) Class I (also cknown as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CHLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) c.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 6
Cytotoxic T lymphocyte epitopic peptide p214K9; hepatitis C virus; NS3; NS4; NS5a; NS5b; p214K9; immune response; CTL; HCV; hepatitis C virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                 Cytotoxic T Lymphocyte
                                                                                                     02-AUG-2001
                                                                                                                                       AAB98703
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551214/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                   AAB98703 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                produce CTLs ex vivo for infusion back into a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides enco
                                                                                                                                                                                                                                                                                          145 SPGQRV 150
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenic peptides with HLA binding motif, useful in treatment diagnosis of cancers and viral diseases \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to AAY48214 represent specifically claimed immunogenic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 128; 150pp; English.
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the immunogenic peptides are also useful and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                          2.1%; Score 6; DB 20; L
100.0%; Pred. No. 4.3e+05;
Live 0; Mismatches 0;
                                                                epitopic peptide p214K9 from hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 either an NS3, NS4 and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and NS5b polypeptide of earliested immune responses, e.g. activating HCV-specific T cells. The fusion protein is useful for generating an immune response against HCV in a mammal, particularly a cytotoxic T lymphocyte (CTL) response for either therapeutic or prophylactic treatment against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein will activate CD8+ cells which recognise and lyse target cells displaying an NS5a epitope. The present sequence was useful in the production of the invention which includes fusion proteins comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents cytotoxic T lymphocyte epitopic peptide p214K9 which comes from hepatitis C virus NS5a protein (HCV-NS5a), this sequence was used in an experiment of the invention to show that immunisation with plasmid or naked DNA encoding an NS3NS4NS5a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus (HCV) polypeptides and fusion proteins, useful for stimulating cell-mediated immune responses, particularly for therapeutic or prophylactic treatment against HCV infection hepatitis C
19-JUL-1999;
                                                                                    WO200121189-A1
                                                                                                                                              antiviral
                                                                                                                                                           Hepatitis C virus;
                                                                                                                                                                                      Hepatitis C virus epitope #153
                                                                                                                                                                                                                    02-JUL-2001
                                                                                                                                                                                                                                                  AAJ00162;
                                                                                                                                                                                                                                                                              AAJ00162 standard; Peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                          19-JUL-2000; 2000WO-US19774.
                                                                                                                Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                  46 EYPVGS 51
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2 eypvgs 7
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6; Conser
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ilarity 100.0%;
Conservative
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99US-0357737
                                                                                                                                                         HCV; epitope; vaccine;
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Pred. No.
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. 4.3e+05;
                                                                                                                                                            immunogen; HLA-binding motif;
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Baker DM,
                                                                                                                  WPI;
Sequence
                 The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                             Disclosure;
                                                                                                                                                                                                        19-JUL-2000;
                                                                                                                                                                                                                           29-MAR-2001
                                                                                                                                                                                                                                              WO200121189-A1
                                                                                                                                                                                                                                                                 Hepatitis C virus
                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding
                                                                                                                                                                                                                                                                                                                Hepatitis C
                                                                                                                                                                                                                                                                                                                                    02-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new composition useful as a vaccines
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                                                                                                                                                                                                                                                                                                                                                                          AAJ00288 standard;
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nes 6; Conserv
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| 2 spgqrv 7
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                                                                                                                                      DM,
                                                                                               composition
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                                                                                                                                     Sidney J,
Celis E,
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Celis E,
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                                                                            Page 107;
                                                                                                                                                                                                                                                                                                                virus
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                                                                                                                                                                                     99US-0357737
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                                                                                               useful as a vaccines
                                                                                                                                                                                                                                                                                                               epitope #279
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100.0%;
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                                                                                               against hepatitis
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Matches 6; Conserv
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                                                                                                                                                                                                                                           The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HIA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
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Baker
                           Hepatitis C
                                              02-JUL-2001
                                                                                    AAJ01463
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                      Disclosure; Page 129; 214pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiviral
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Celis E,
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                          virus epitope #1454.
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100.0%;
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Hepatitis C antiviral.

virus;

HCV; epitope;

vaccine;

immunogen;

HLA-binding

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Disclosure; Page 144; 214pp; English
                                                                                        A new composition useful as a vaccines against hepatitis
                                                                                                                                                                                WPI; 2001-308046/32
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Kubo RT, Grey HM;
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                                                                                                                         The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AaJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
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antiviral.
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                             (first entry)
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          99US-0357737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0357737
                                                                                                           HCV;
                                                                                                                                                                                  Peptide;
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                                                                                                                                                                                                                                                                            2.1%;
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Kubo RT, Grey HM;
                                                                                                           epitope;
                                                                                                                                                                                  9 AA
                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                            Score 6;
Pred. No.
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Livingston BD,
                                                                                                                                                                                                                                                                            DB 22; Lo
                                                                                                                                                                                                                                                                                                                                                                                                        against hepatitis
                                                                                                           immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen; HLA-binding motif;
                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chesnut
                                                                                                           HLA-binding
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                                                                                                          motif;
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Best Local S
Matches 6
                                                                                                                                                          Sette A,
Baker DM,
                    The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ0010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                     Sette
                                                                                                              A new composition useful as a vaccines against hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a composition comprising a prepared hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121. These are derived from HCV HLA-binding motifs. They are useful in vaccines for the prevention and treatment of HCV infection in humans. The present sequence is an epitope used in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sette
Baker
Sequence
                                                                                        Example 2;
                                                                                                                                     WPI; 2001-308046/32
                                                                                                                                                                                                                  19-JUL-1999;
                                                                                                                                                                                                                                                                29-MAR-2001
                                                                                                                                                                                                                                                                                      WO200121189-A1
                                                                                                                                                                                                                                                                                                                                   Hepatitis C
antiviral.
                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus epitope #3892.
                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                AAJ03901;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAJ03901 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A new composition useful as a vaccines against hepatitis
                                                                                                                                                                                            (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                         19-JUL-2000; 2000WO-US19774
                                                                                                                                                                                                                                                                                                            Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 185; 214pp;
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Celis E,
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Celis E,
                                                                                        Page 193; 214pp;
9
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ΑA;
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                                                                                                                                                                                                                                                                                                                                              HCV;
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100.0%;
                                                                                                                                                          Southwood Kubo RT,
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                                                                                                                                                                                                                                                                                                                                             epitope;
                                                                                        English
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Pred. No.
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                                                                                                                                                          S, Livingston Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                             vaccine; immunogen;
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                                                                                                                                                                      BD,
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                                                                                                              virus
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Query Match

2.1%;

Score

6

DB 22;

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9;

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AAY49753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                           CC A composition (A) comprises at least a first dimerisation peptide (I)

CC comprising the sequence (S1) that is no more than 8 amino acids long,

CC where the composition optionally comprises a second dimerisation peptide

CC (II): NH2-X1-X2-X3-X4-X5-COOH (S1) where X1 to X4 = Ala, Val, Ile, Ieu,

CC TIP, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu;

CC NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are

CC displayed intracellularly or extracellularly and are useful to identity

CC binding proteins and molecules, and to modulate intracellular signalling

CC its bloactive potential. The invention can be used to access molecules

CC or targets within living cells, and then provide for the isolation of

CC the constrained protein which has a phenotypic effect on the living

CC cells. The methods are also useful to identify in vitro binding partners

CC of the constrained protein. The compositions of the invention are useful

CC as a scaffold for gene therapy and for potential use as a therapeutic

CC in physiological fluids. The present sequence is used in the
                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes peptides which have a moderate or high affinity for each other, when added as extensions to both the N-terminus and C-terminus of a protein, can be used to help fold the protein into a compact structure. This compact structure is more stable to proteases.
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 18; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel dimerization peptides which self-associate are used with other proteins to effect the formation of compact structures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-620191/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compact structure forming peptide; dimerisation; stability; scaffold; library screening; drug screening; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compact structure forming exemplification peptide #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49753 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9951625-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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241 VQRKRQ 246
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                                                       2.1%; Score 6; DB:
ilarity 100.0%; Pred. No. 79
Conservative 0; Mismatches
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5. 79;
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0; Gaps 0;

Search completed: January 24, 2002, 16:25:45

Job time: 130 sec
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OM protein - protein search, using sw model
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                                       GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd
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          US-08-595-59-5

US-08-928-958-5

US-09-072-429-5

US-08-392-816-9

US-08-132-164-1

US-08-098-142A-8
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PCT-US95-13841-2
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US-07-817-916A-1
US-08-003-839-1
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US-08-789-333F-9
US-09-169-015-19
US-09-133-944-9
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5204326-84
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Sequence 9, Appli
Sequence 19, Appli
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Database :

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sequence 205, App		Sequence 10, Appl	Sequence 10, Appl	Sequence 149, App	Sequence 90, Appl	Sequence 19, Appl	Sequence 19, Appl	Sequence 19, Appl	Sequence 184, App	Sequence 6, Appli	Sequence 4, Appli	Sequence 503, App	Sequence 4, Appli	Sequence 670, App	Sequence 9, Appli	•	Sequence 429, App

## ALIGNMENTS

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US-08-789-333F-9

Sequence 9, Application US/0878933F

Patent No. 6153380

GENERAL INFORMATION:
APPLICANT: No. 6153380an, Garry P

APPLICANT: Rothenberg, S. M.

TITLE OF INVENTION: METHODS FOR SCREENING FOR TITLE OF INVENTION: EFFECTOR PEPTIDES AND RN.

FILE REFERENCE: A642601DJBRMSDSS
CURRENT APPLICATION NUMBER: US/08/789,333F

CURRENT FILING DATE: 1997-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haaf, Thomas
APPLICANT: Haaf, Thomas
APPLICANT: Reddy, Gurucharan
APPLICANT: Redding, Charles M.
APPLICANT: Radding, Charles M.
APPLICANT: Ward, David C.
APPLICANT: Ward, David C.
FILE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING RAD51
FILE REFERENCE: A-65680/RFT/RMS
FILE REFERENCE: A-65680/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-05-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application Patent No. 6090539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/007,020 CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,834 EARLIER FILING DATE: 1997-01-30 EARLIER APPLICATION NUMBER: 60/045,668 EARLIER APPLICATION NUMBER: 60/045,668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides; FILE REFERENCE: A6690/DJB/RWS/SJR
CURRENT APPLICATION UMBER: US/09/169,015; CURRENT FILING DATE: 1998-10-08; NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH. 10
                                                                                                                                                US-09-133-944-9
; Sequence 9, Application US/09133944
; Patent No. 6280937
; GENERAL INFORMATION:
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APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252/DJB/DAV
CURRENT APPLICATION NUMBER: US/09/133,944
CURRENT FILING DATE: 1999-08-14
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
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SEQ ID NO 9
LENGTH: 10
TYPE: PRT
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Best Local S
Matches 6
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Best Local Similarity
Matches 6; Conserv
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PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                ISSUE: 64
PAGES: 961-
DATE: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens PUBLICATION INFORMATION: JOURNAL: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1996-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1
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                                                                                                                                                                                                                                                                                                             241 VQRKRQ 246
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100.0%; Pred. No. 26;
tive 0; Mismatches
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100.0%; Pred. No. 26;
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RESULT 6
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5204326-81
; Patent No. 5204326
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                                                                                                                                                                                                                              ;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YANAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI,TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-133-944-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HETABOLISM IMPROVING AGENT
NUMBER OF SEQUENCES: 147
CURRENT APPLICATION DATA:
                                                                                                                        FILING DATE: 14-MAR-1990
SEQ ID NO:82:
                                                                                                                                                                                           METABOLISM IMPROVING AGENT NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMEA, SHIZUO; HIROHASHI, MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHII TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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SOFTWARE: PatentIn Ver. SEQ ID NO 9
                Query Match
Best Local S
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Best Local Similarity
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JOURNAL: Cell
VOLUME: 62
PAGES: 1019-1019
DATE: 1990
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Similarity
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100.0%; Pred. No.
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2.1%; Score 6; DB (
100.0%; Pred. No. 30)
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RESULT 8
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                                                                                                                                                                                                      Sequence 1, Application US/07817916A Patent No. 5252467
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Chang, Tse Wen
TITLE OF INVENTION: Making antibodies to antigenic epitopes present on B cell but
TITLE OF INVENTION: surface
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REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TN:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 664-2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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APPLICATION NUMBER: 07/
FILING DATE: 11/16/1988
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: DNA encoding antibodies to antigenic epitopes present on B
TITLE OF INVENTION: basophil surface
                                                                                                    CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
SOFTWARE: Wordper!
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                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                            247 EAEGEA 252
                                   CITY: Houston
STATE: Texas
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CLASSIFICATION: 435
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COUNTRY: USA
ZIP: 77025
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                                                                                    ADDRESSEE:
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                                                                   E: Tanox Biosystems, Inc
10301 Stella Link Rd.
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(713) 664-801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5292867
Patent No. 5292867
GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS 3.30 SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION: TELEPHONE: (713) 664-2288
                                                                            APPLICATION NUMBER: 07/817,918
FILING DATE: 1/6/92
APPLICATION NUMBER: 07/272,243
FILING DATE: 11/16/1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Peptides representing antigenic epitopes present on B cell TITLE OF INVENTION: surface
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REFERENCE/DOCKET NUMBER: TN
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
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nes 6; Conserv
                                               NAME: Mirabel, Eric P. REGISTRATION NUMBER: 3
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ZIP: 77025
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FILING DATE: 11/16/1988
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                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/003,839
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10301 Stella Link Rd.
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                                 TNX88-03BBB
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TYPE: amino acids
TOPOLOGY: linear
US-08-003-839-1
RESULT 11
5204326-83
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
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PCT-US93-06278-1
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/468,766

APPLICATION NUMBER: 01/23/1990

ATTORNEY/AGENT INFORMATION:

NAME: Mirabel, Eric P.

REGISTRATION NUMBER: 31,211

REFERENCE/DOCKET NUMBER: TNX88-0

TELEPHONE: (713) 664-2288

TELEPHONE: (713) 664-8914

INFORMATION FOR SED ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRESENT ON B CELL BUT NOT BASOPHIL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chang, Tse Wen
                                                                                                                                          247 EAEGEA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: POFILING DATE: 19930701 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 10301
CITY: Houston
                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                              8 EAEGEA 13
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                                                                                                                                                                       2.1%; Score 6; DB ilarity 100.0%; Pred. No. 34. Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                       linear
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100.0%; Pred. No. 34;
tive 0; Mismatches
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RESULT 13
5204326-89
;PATENT NO. 5204326
; PATENT NO. 5204326
; APPLICANT: FUJII, SETSURO:YAMAMOTO, YOSHIHITO:SHIMIZU, FUMIO; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI, MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM;
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Best Local Similarity
Thes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5204326-83
                                                                                                                                                                                         FILING DATE: 14-MAR-1990
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; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5204326-84
;Patent No. 5204326
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APPLICATION NUMBER: US/07/493,359
FILING DATE: 14-MAR-1990
;SEQ ID NO:83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; METABOLISM IMPROVING AGENT 
; NUMBER OF SEQUENCES: 147
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                                                                                                                                                                                                                                                                 METABOLISM IMPROVING AGENT NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conser
                                                                   Matches
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Best Local Similarity
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                                 15 TPRTDV 20
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4 TPRTDV 9
5 TPRTDV 10
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100.0%; Pred. No.
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0; Mismatches
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o. 34;
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RESULT 14
5204326-85
;Patent NO. 5204326
; Patent NO. 5204326
; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION NUMBER: US/07/493,359
;FILING DATE: 14-MAR-1990
;SEQ ID NO:85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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5204326-85
; TOPOLOGY: 1; MOLECULE TYPE: PCT-US95-13841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-13841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9513841
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1
Best Local Similarity 100
Matches 6; Conservative
                                                                    TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/328,519

FILING DATE: 25-OCT-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C.H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4117

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-OCT CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U. ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: NY
                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TPRTDV 20
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                                       linear
              peptide
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Pred. No.
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Query Match

2.18;

Score 6;

DB 5;

Length 17;

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Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 247 EAEGEA 252
||||||
Db 9 EAEGEA 14
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Search completed: January 24, 2002, 16:26:05 Job time: 150 sec

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Result
No.
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Maximum DB
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                                                                                                                                                                    Score
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seq length:
        6677
6677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-741-095B-26
283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEPPGDWGPPPWRSTPRTDV.....VTTVAVEETIPSFTGRSPNH
                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
/cgn2_6/ptodata/2/paa/US092_COMB.pep:*
/cgn2_6/ptodata/2/paa/US093_COMB.pep:*
/cgn2_6/ptodata/2/paa/US093_COMB.pep:*
/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
/cgn2_6/ptodata/2/paa/US087_COMB.pep:*
/cgn2_6/ptodata/2/paa/US087_COMB.pep:*
/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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 PCT-US99-20180-51
7 US-09-342-767-51
PCT-US99-20180-50
17 US-09-342-767-50
18 US-09-342-767-50
19 US-09-724-059-21780
10 US-09-724-059-314140
10 US-09-357-737-1617
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820.990 Million cell updates/sec
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Sequence 51, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 21, Appl
Sequence 21780, A
Sequence 34140, A
Sequence 1066, Ap
Sequence 1617, Ap
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****	-60-161-713-1	09-357-737B-25	US-09-357-737B-1734	us-09-357-737B-1673	-357-737B-137	7-737B-1	9-357-737B-20	US-09-357-737B-77	7-737A-3	9-357-737A-3	-09-357-737A-252	-09-357-737A-1	-09-357-737A-167	-09-357-737A-13	-09-357-737A-10	US-09-357-737A-203	-09-357-737A	-09-357-737-	US-09-357-737-3387	-09-	US-09-357-737-1734	US-09-357-737-1673	US-09-357-737-1378	-09-357-737-1	7-20	-09-357-737-77	-09-017-743C-8	43A-	-08-344-824A	-08-344-824-10	08-278-634-9	-US00-23913-8	-09-357-737B-	-09-357-737B-106	-09-357-737A-	US-09-357-737A-1066
sequence I, April		e 2529,	e 1734,	Sequence 1673, Ap	e 1378,	e 1067,	e 203,	Sequence 77, Appl	e 3664	е 3387,	2529,	e 1734,	e 167	1378,	1067,	203,	e 77, Ap	3664,	e 3387,	e 2529,	e 173	e 1673,	e 1378,	1067,	203,	77,	82,	e 82,	95,	10	90,	82, App	e 1617,		1617,	,

## ALIGNMENTS

CURRENT APPLICATION NUMBER: PCT/US99/20180
CURRENT FILLING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILLING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILLING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 25 멍 QΥ ; TYPE: PRT; ORGANISM: Homo sapiens PCT-US99-20180-51 PCT-US99-20180-51 Sequence 51, Application PC/TUS9920180
GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 09404/079W01 Query Match Best Local Similarity Matches 25; Conserv 201 WVWWFLSGSLVIVIVCSTVGLIICV 225 1 WVWWFLSGSLVIVIVCSTVGLIICV 25 Conservative 100.0%; 8.8%; Score 25; Pred. No. 0; Mismatches Inc.
THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED DB 1; 9.9e-17 THEREOF Length 25 0, 0

US-09-342-767-51

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                                                                                                                                                                                     US-09-342-767-50
                                                                                                                                                                                                           RESULT
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LENGTH: 22
TYPE: PRT
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APPLICANT: MIllennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERDESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
EILE REFERENCE: 09404/079901
                                                                                                                                        Sequence 50, Applica GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserv
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SEQ ID NO 51
LENGTH: 25
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Best Local Similarity '100.0%; Pred. No.
Matches 22; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US99/20180 CURRENT FILING DATE: 1999-09-03 EARLIER APPLICATION NUMBER: 05/342,767 EARLIER FILING DATE: 1999-06-29 EARLIER APPLICATION NUMBER: US 09/146,950 EARLIER FILING DATE: 1998-09-03
                               TITLE OF INVENTION: NOVEL MOLECULES OF THE TITLE OF INVENTION: HERPESVIRUS-ENTRY MEDIATOR-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: MBIO98-061CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: US 09/146,950 EARLIER FILING DATE: 1998-09-03 NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1999-06-29
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TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/342,767
                                                                                                                    APPLICANT: Busfield, Samantha J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Busfield,
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                                                                                                                                                              Application US/09342767
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100.0%; Pred. No.
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8.6e-14;
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9.9e-17;
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RESULT

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LENGTH: 22
TYPE: PRT
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                                                            Matches
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Best Local Similarity
                                                                                        Query Match
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                                                                                                                                                                                                                                                                        FILING DATE:
CIASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                              TELEFAX: (301) 309-84.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,582
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                             263 DYTTVAVEETIPSFT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 CPPGTFSPNGTLEECQHQTKCS 186
                                                          Local Similarity
nes 15; Conserv
                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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9410 KEY WEST AVENUE
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                                                            Conservative
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100.0%;
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[00.0%; Pred. No.
                                                                           Score 15; pred. No.
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                                                            Mismatches
                                                                           DB 14;
. 5.7e-07;
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                                                          Gaps
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US-09-724-059-21780

Sequence 21780, App GENERAL INFORMATION

Application US/09724059

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Query Match
Best Local Similarity
7; Conserve
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Best Local Similarity
7; Conserve
                                                                                           US-09-357-737-1066
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                                                                                                               RESULT
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                                                               GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 1407122
SOFTWARE: MacAllLister
SEQ ID NO 21780
LENCTH: 25
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MacAllLister
SEQ ID NO 34140
LENGTH: 25
                                                                             Sequence 1066, Application US/09357737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Isalan, Mark
TITLE OF INVENTION: Nucleic Acid Binding Proteins
FILE REFERENCE: P2500USM
CURRENT APPLICATION NUMBER: US/09/724,059
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Isalan, Mark
TITLE OF INVENTION: Nucleic Acid Binding Proteins
FILE REFERENCE: P2500USM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/724,059
CURRENT FILING DATE: 2000-11-28
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                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB9710809.6 PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1407122
                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                    FEATURE:
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14 RTDVLRL 20
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RTDVLRL 20
                                                 Sette, Alessandro
Sidney, John
Southwood, Scott
Livingston, Brian
                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                     2.5%;
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100.0%; Pred. No.
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                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                       Score 7;
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5.86;
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5.86;
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Best Local Similarity
Watches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-357-737-1617
                                                                            PRIOR APPLICATION NUMBER: U.S.S.N.
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 3681
SOFTWARE: FASTSEQ for Windows Versi
SEQ ID NO 1617
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ORGANISM: Hepatitis C Virus -09-357-737-1617
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: U.S.S.N. 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR PILING DATE: 1993-11-29
PRIOR PILING DATE: 1993-10-04
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-06-04
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PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID (FILE REFERENCE: 18623-014000US
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                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/357,737
CURRENT FILING DATE: 1999-07-19
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PRIOR PILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
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CURRENT FILING DATE: 1999-07-19
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TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
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                                          TYPE: PRT
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Best Local Similarity
"hes 6; Conserve
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PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
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Best Local Similarity
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TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 18623-0144000US
CURRENT APPLICATION NUMBER: US/09/357,737A
CURRENT FILING DATE: 1999-07-19
FILE REFERENCE:
             TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS
TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
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                                                                                         Baker,Denise
Celis,Esteban
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Celis,Esteban
                                                    Grey, Howard
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18623-014000US
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US-09-357-737A-1617
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PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
PRIOR FILING DATE: 1993-03-05
                                                                                                                                                                                               SOFTWARE: Fast
SEQ ID NO 1066
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LENGTH: 8
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
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PRIOR APPLICATION NUMBER: US 08/159,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C TITLE OF INVENTION: Virus Using Peptide and Nucleic Acid Compositions FILE REFERENCE: 018623-014000US
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                                                                                                                                     ORGANISM: Hepatitis
                                                                                                                                                          TYPE: PRT
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Epimmune Inc.
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SOFTMARE: FastSEQ for with the soft No. 82
SEQ ID NO. 82
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
"~+~hes 6; Conserva
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; OTHER INFORMATION: HIV NS5 2615, peptide 1292.23 PCT-US00-23913-82
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                                                                                                                                                                   APPLICANT: Epimmune Inc.
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 18623-80-5PC
CURRENT APPLICATION NUMBER: PCT/US00/23913
CURRENT FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                  NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 3683
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
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TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C
TITLE OF INVENTION: Virus Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 018623-0140005
                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/357,737B CURRENT FILING DATE: 1999-07-19
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100.0%; Prr
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NO. 2.9e+06;
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Search completed: January 24, 2002, 16:28:09 Job time: 184 sec

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US-08-278-634-90
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GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
                                                              Query Match
Best Local Similarity
Matches 6; Conser
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Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                 TELEFAX: 415/543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/278
FILING DATE: 21-JUL-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew.
STREET: One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                 MOLECULE TYPE:
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                               145 SPGQRV 150
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 2.
Live 0; Mismatches
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100.0%; Pred. No.
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                       /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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US-08-816-011E-10
US-08-816-011E-10
US-09-881-636-33
US-09-881-636-339
US-09-881-636-339
US-09-881-636-633
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Ouery Match  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 22;  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gap  Qy 241 VQRKRQ 246              Db 3 VQRKRQ 8  RESULT 2  US-09-572-404B-1338 ; Sequence 1338, Application US/09572404B ; GENERAL INFORMATION: ; APPLICANT: Proteom Ltd ; TITLE OF INVENTION: Complementary peptide ligands from the human geno	OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULE EFFERNCE: A-64260-6/RMS/MAS T APPLICATION NUMBER: US/09/916,940 T FILING DATE: 2001-07-27 APPLICATION NUMBER: US 09/727,715 FILING DATE: 2000-11-28 APPLICATION NUMBER: US 08/963,368 FILING DATE: 1996-01-23 APPLICATION NUMBER: US 08/589,919 FILING DATE: 1996-01-23 APPLICATION NUMBER: US 08/789,333 APPLICATION NUMBER: US 08/789,333 FILING DATE: 1997-01-23 APPLICATION NUMBER: US 08/787,738 FILING DATE: 1997-01-23 OF SEQ ID NOS: 102 OF SEQ ID NOS: 102 RE: PATENTIN Ver. 2.0 NO 9 PRT ISM: Artificial Sequence INFORMATION: Description of Artificial Sequence: INFORMATION: localization sequence: -940-9	ALIGNMENTS  ESULT 1 S-09-916-940-9 Sequence 9, Application US/09916940 GENERAL INFORMATION: APPLICANT: NOLan, Garry P TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELI	27 5 1.8 10 5 US-09-572-404B-1580 Sequence 158 US-09-572-404B-3020 Sequence 370 Sequence 371 Sequence 372 Sequence 373 Sequence 373 Sequence 373 Sequence 373 Sequence 373 Sequence 373 Sequence 374 Sequence 375 Sequence 375 Sequence 376 Sequence 377 Sequence 378 Seq
Gaps 0;		EL	

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GENERAL INFORMATION:

APPLICANT: Pausch, Mark H

APPLICANT: Price, Laura A

TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

TITLE OF INVENTION: AND METHODS OF USING SAME

FILE REFERENCE: 01142.0122 SEQUENCE LISTING

CURRENT APPLICATION NUMBER: US/08/816,011E

CURRENT FILING DATE: 1997-03-11

PRIOR APPLICATION NUMBER: 08/332,312

PRIOR FILING DATE: 1994-10-31

PRIOR APPLICATION NUMBER: POT/US95/14364

PRIOR FILING DATE: 1995-10-25

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 24
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US-08-816-011E-10
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                                                                                                                             Sequence 18, Application US/08816011E
GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011E
CURRENT FILING DATE: 1997-03-11
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 67
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100.0%; Pred. No. 46;
tive 0; Mismatches
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100.0%; Pred. No.
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Query Match
Best Local Similarity
~~+~hes 6; Conserve
; ORGANISM: Drosophila melanogaster US-08-816-011F-18
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US-08-816-011F-10
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                                  NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 24
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08816011F GENERAL INFORMATION:
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PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 24
TYPE: PRT
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Best Local Similarity
Matches 6; Conserv
                                                                                                                              TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011F
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Pausch, Mark H APPLICANT: Price, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, TITLE OF INVENTION: AND METHODS OF USING SAME FILE REFERENCE: 0.1142.0122 SEQUENCE LISTING CURRENT APPLICATION NUMBER: US/08/816,011F. CURRENT FILING DATE: 1997-03-11 PRIOR APPLICATION NUMBER: 0.8/33,312 PRIOR FILING DATE: 1994-10-31
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100.0%; Pred. No. 46; 
1ve 0; Mismatches
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Pred. No.
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-38
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; LOCATION: (1)..(7)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-17
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Sequence 17, Application PC/TUS0128124A
Sequence 17, Application PC/TUS0128124A
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Biopanning and Rapid Anaylsis of Selective Interactive Ligands;
FILE REFERENCE: 005774.P004PCT
CURRENT APPLICATION NUMBER: PCT/US01/28124A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 289
COUNTRING SEQ ID NOS: 289
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Best Local Similarity 100.0%;
Matches 5; Conservative (
                                   Query Match 1.8%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 5; Conservative 0; Mismatches
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Best Local Similarity
Matches 6; Conserv
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 55P414: GENE EXPRESSED IN VARIOUS TITLE OF INVENTION: CANCERS FILE REFERENCE: 129.12USU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mary Faris APPLICANT: Rene S. H
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NUMBER OF SEQ ID NOS: 720
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ORGANISM: Artificial Sequence
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3 LSGSL 7
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   19 DVLRL 23
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Steve Chappell Mitchell
Arthur B. Raitano
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100.0%; Pred. No. 46;
tive 0; Mismatches
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100.0%; Pred. No.

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                                                                                                                                             ; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-128
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                                                                                                                                                                                                                                                 APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 55P4H4: GENE EXPRESSED
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR APPLICATION NUMBER: 50/211,454
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 720
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                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
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APPLICANT: Rene S. H
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19 DVLRL 23
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Daniel E.H. Afar
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Steve Chappell Mitchell
Arthur B. Raitano
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Daniel E.H. Afar
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100.0%;
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                                                  score 5; DB 5; Pred. No. 1.4
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Best Local Similarity
Thes 5; Conserve
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                                 Matches
                                                                              Query Match
Best Local :
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SEQ ID NO 236
LENGTH: 9
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USUI
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
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PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 720
SOFTWARE: Factor
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION: CANCERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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nes 5; Conserv
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Daniel E.H. Afar
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Daniel E.H. Afar
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                                                               Conservative
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Вþ
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Best Local Similarity 100.
Ches 5; Conservative
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 532
LENGTH: 9
TYPE: PRT
                                                                             Query Match
Best Local :
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SEQ ID NO 426
LENGTH: 9
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,454
PRIOR FILING DATE: 2000-06-13
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TITLE OF INVENTION: 55P4H4: GENE EXPRESSI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
CURRENT APPLICATION NUMBER: US/09/881,636
CURRENT FILING DATE: 2001-06-13
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APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
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TITLE OF INVENTION: CANCERS
FILE REFERENCE: 129.12USU1
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APPLICANT: Rene S. Hubert
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Steve Chappell Mitchell
Arthur B. Raitano
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US-09-881-636-633
Sequence 633, Application US/09881636
Sequence 633, Application US/09881636
Sequence 633, Application US/09881636
GENERAL INFORMATION:
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Atchur B. Raitano
APPLICANT: Atchur B. Raitano
APPLICANT: Applicant ON Spi44: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION: 55944: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION: SP44: GENE EXPRESSED IN VARIOUS
TITLE OF INVENTION UNMERR: US/09/881,636
CURRENT APPLICANTON UNMERR: 00/211,454
PRIOR FILLING DATE: 2000-06-13
PRIOR APPLICANTON UNMERR: 60/211,454
PRIOR FILLING DATE: 2000-06-13
INMBER OF SEQ ID NOS: 720
SOFTMARE: FASTSEDQ FOR WINDOWS VERSION 4.0
SOFTMARE: FASTSE
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re greater than or equal to the score of the result being printed,
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length: 30
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283
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B43590
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## ALIGNMENTS

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence\_revision
C:Accession: PT0715

17-Jul-1992 #text\_change 30-May-1997

RESULT 1
PT0715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)

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Query Match
Best Local Similarity
~~+ches 5; Conserv
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Infect. Immun. 59, 3478-3483, 1991
A:Title: Purification and characterization of A; Reference number: A43590; MUID:91372953
A; Accession: B43590
                                                                                                                                                                                                                                                             RESULT 2

843590

943590

pilin type Ae6 - Aeromonas hydrophila (fragment)

C:Species: Aeromonas hydrophila

C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 17-Nov-2000

C:Accession: B43590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601
A;Accession: PT0715
A;Accession: PT0715
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                                                                                                              A; Molecule type: protein A; Residues: 1-10 <HOK> C; Superfamily: Vibrio che
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Best Local Similarity
"-+-hes 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-6 <PEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell'receptor
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210 LVIVI 214
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o. 2.2e+02;
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В

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A; Molecule type: protein A; Residués: 1-10 < RAM> R; Kawakami, T.; Ts submitted to JIPID, March 19 A; Reference number: PA0109 A; Accession: PA0107
                                                                                               R; Harriott)
Gene 161, 6
                                            A; Title: Sequences of nifx, A; Reference number: JC4203; A; Accession: PC4055
                                                                                                C;Species: Frankia sp.
C;Date: 10-Sep-1995 #sequence_revision
C;Accession: PC4055
R;Harriott; O.T.; Hosted, T.J.; Benson,
Gene 161, 63-67, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pilin type Ae1 - Aeromonas sobria (fragment)
C:Species: Aeromonas sobria
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 18-Jun-1993
               A; Molecule type: DNA
A; Residues: 1-13 <HAR>
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A; Accession: PA0050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein QA100052 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0050; PA0107
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A; Accession: A43590
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Infect. Immun. 59, 3478-3483, 1991
A; Title: Purification and characte
A;Cross-references: GB:L29299
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Matches 5; Conserv
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2.2e+02;
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                                                                                  two
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PH0773
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pilin - Aeromonas sobria (fragment)
C;Species: Aeromonas sobria
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: T cell receptor genes in a series of class I major histocompatibility comple allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0773
A;Reference number: A47678; MUID:93018994 A;Contents: TAP13
                                       A; Title: Characterization of Aeromonas sobria TAP13 pili: a possible new colonization
                                                       R; Iwanaga, M.; Hokama, A.
J. Gen. Microbiol. 138, 1913-1919, 1992
                                                                                                 C; Accession: A47678
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Whiches 5; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-16 <CAS2
A;Cross-references: EMBL:X60868; NID:g50247; PIDN:CAA43257.1;
A;Experimental source: T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  κ;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J.Exp. Med. 174, 1371-1383, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: PH0773
R;Casanova, J.L.; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell receptor beta chain (C7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
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Best Local Similarity
Watches 5; Conserv:
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A;Molecule type: protein
A;Residues: 1-15 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S14749
R;Chaudhuri, S.; Duncan, K.; Graham, L.D.; Coggins, J.R.
Biochem. J. 275, 1-6, 1991
A;Title: Identification of the active-site lysine residues of two biosynthetic 3-dehy A;Reference number: S14749; MUID:91207275
A;Accession: S14749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-dehydroquinase - Neurospora crassa (fragment)
C;Species: Neurospora crassa
C;Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
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Best Local Similarity
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5. 3.1e+02
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b. 2.7e+02;
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photosystem I 14.0K E4 chain - common tobacco (fragment) C:Species: Nicotiana tabacum (common tobacco) C:Date: 19-May-1994 *sequence_revision 19-May-1994 *text
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-17 - CIWA>
A;Note: sequence extracted from NCBI backbone (NCBIP:116639)
A;Note: sequence extracted from Propilin-like 17.3K protein type
photosystem I 14.1K E3 chain
C; Species: Nicotiana tabacum
                                   PQ0687
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A;Tille: Molecular heterogeneity of photosystem I. psaD, psaE, p. A;Reference number: PQ0667; MUID:94105345
                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: PQ0688
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Best Local Similarity
"~+~hes 5; Conserv
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A;Description: Conservation of a methylation imprint and a putative imprinting
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                                                     RESULT 11
                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-20 <080>
                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: PQ0688
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A; Residues: 1-18 <SMR>
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A; Accession: S58277
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C;Accession: S58277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                               Matches
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Keywords: growth factor
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                                                                                                                                            248 AEGEA 252
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                                                                                                           AEGEA
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                    photosynthesis;
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 (common tobacco)
                  common
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; Pred. No. 3.6
0; Mismatches
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Pred. No.
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Pred. No.
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                tobacco
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o. 4e+02;
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b. 3.5e+02;
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. 3.6e+02;
ches 0; Indels
                (fragment)
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                                                                                                                                                                                                             Length 20;
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C;Genetics:
                                                   A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-21 <RES>
                                                                                                               A; Reference number: I58423; MUID:95218835
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 5; Conserve
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A; Residues: 1-21 <RES2
A; Cross-references: GB: M34478; NID:g143851; PIDN:AAA98049.1; PID:g143852
C; Superfamily: tetracycline resistance protein
C; Keywords: antibiotic resistance; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetracycline resistance (tet) protein - plasmid pBC16 (fragment)
C;Species: plasmid pBC16
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, Plant Physiol. 102, 1259-1267, 1993 A;Tille: Molecular heterogeneity of photosystem I. I A;Reference number: PQ0667; MUID:94105345 A;Accession: PQ0687
                                                                                                                                                             R; Mimura, J.; Ema, M.; Sogawa, K. Pharmacogenetics 4, 349-354, 1994
                                                                                                                                                                                                             C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appl. Environ. Microbiol. 56, 1128-1134, 1990 A;Title: Expression of Bacillus thuringiensis A;Reference number: 140157; MUID:90253151 A;Accession: 140157
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C;Accession: PQ0687; PQ0675
                                     A; Cross-references:
                                                                                                         A; Accession: I58423
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                                                                                                                                                                                                                                                                                        RESULT
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Best Local
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R;Kreil, G. 1975
FEBS Lett. 54, 100-102, 1975
A;Title: The structure of Apis dorsata melittin: phylogenetic relationships between hone A;Reference number: A01763; MUID:75168194
A;Recession: A01763
A;Accession: A01763
A;Molecule type: protein
A;Residues: 1-26 (KRE)
C;Superfamily: melittin major
C;Superfamily: melittin major
C;Keywords: amidated carboxyl end; homotetramer
F;26/Modified site: amidated carboxyl end (Glu) #status experimental
Search completed: January 24, 2002, 16:26:28 Job time: 113 sec
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C;Species: Apis mellifera dorsata (giant honeybee)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000
C;Accession: A01763
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C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Zeke, T.; Gergely, P.; Dombradi, V. submitted to the EMBL Data Library, July 1996
A;Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditi A;Reference number: 222131
A;Reference number: 222131
A;Accession: T42257
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ilarity 100.0%; Pred. No. 4.7e+02;
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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283
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 DB
TERM_BPM2
UC19_MAIZE
HBD_CLOPA
YPFK_SALTY
CHP_THICU
COG2_CHIOP
COG3_CHIOP
COGA_PARCM
COGB_PARCM
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HTF1_ENCAM
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HTF_TENAM
HTF_TENAM
CYPCA
OXYT_CYPCA
OXYT_SQUAC
CCXH_ONCMY
ESL_LACCA
GSO9_BACSQU
TRP5_LEUMA
LFW_THETH
TEMC_RANTE
UP71_LITEM
UP71_LITEM
CALL_CALGI
GLEM_STEGE
PSAG_CUCSA
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P34168 homo sapien
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3 clostridium
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LIT 2 _HUMAN STANDARD; P34158; O1-FEB-1994 (Rel. 28, Crea O1-FEB-1994 (Rel. 28, Last C0-AUG-2001 (Rel. 40, Last C0-AUG-2001 (Rel. 40, Last CHYMOTRYPSIN-LIKE SERINE p Homo saplens (Human). Enkaryota; Metazoa; Chorda Mammalia; Eutheria; Primat NCBI_TaxID-9606; [1] SEQUENCE. TISSUE-Lung; MEDLINE-94092341; PubMed-8 Heidthmann HH., Travis J. "A novel chymotrypsin-like Biol. Chem. Hoppe-Seyler 3 -!- FUNCTION: SPECIFICITY -!- ENZYME REGULATION: INH	llarity Conserva 18	50 E Z C 5 6	STANDARD;  6 (Rel. 34, Cre  6 (Rel. 37, Las  EHYDROGENASE, B  testosteroni (P  Proteobacteria;	
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PRT; 26 AA.  ted) sequence update) annotation update) ROTEINASE (EC 3.4.21. ta; Craniata; Vertebres; Catarrhini; Homin 267879; serine proteinase fr 74:871-875(1993). IBITED BY DFP, TOSYL-	0; Mismatches 0; In	de Vries S., Duine J.A.; swiss-prot data bank. ALDEHYDE + ACCEPTOR + F COMPOSED OF AN ALPHA, A 89BD67D4D05A212E CRC6	MTE STANDARD; PRT; 19 AA.  1996 (Rel. 34, Created)  1996 (Rel. 34, Last sequence update)  1998 (Rel. 37, Last annotation update)  1998 (Rel. 37, Lest annotation update)  100 DEHTDROGENASE, BETA CHAIN (EC 1.2.99.3) (  101 Las testosteroni (Pseudomonas testosteroni).  102 (Las Proteobacteria; beta subdivision; Comamo axID=285;	RIPX_CUCPE  SODE_PASPI  SCIB_BPT5  CT31_LITCI  CR21_LITCI  CR22_LITGI  CR23_LITCE  CR24_LITCE  CR25_LITGI  H2B1_ECHES  MT_AGABI  ALIGNMENTS
-) (LCLP) (FRAGMENT). ata; Euteleostomi; idae; Homo. om human lung."; PHENYLALANYL-	th 19; Indels 0; Gaps 0;	; H(2)0 = AN ACID + BETA AND A GAMMA :54;	9.3) (ALDH) (FRAGMENT). roni). Comamonadaceae: Comamonas.	P80750 cucurbita p P81527 pasteurella P23208 bacteriopha P81851 litoria cit P80919 erythrobact P56233 litoria spl P56234 litoria spl P56235 litoria cae P56236 litoria cae P56237 litoria gil P13281 echinus esc P04358 agaricus bi

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Matches 5
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P01502;
21-JUL-1986
21-JUL-1986
20-AUG-2001
                                                                                                                                                                                                              between honeybees as deduced from sequence data.";
FEBS Lett. 54:100-102(1975)
-I- FUNCTION: MAIN TOXIN OF BEE VENOM WITH STRONG HEMOLYTIC ACTIVITY.
INTEGRATES INTO CELL MEMBRANES AND HAS MULTIPLE EFFECTS, PROBABLY
AS A RESULT OF ITS INTERACTION WITH NEGATIVELY CHANGED
PHOSPHOLIPIDS. IT INHIBITS WELL KNOWN TRANSPORT PUMPS SUCH AS THE
NA(+)-K(+)-ATPASE AND THE H(+)-K(+)-ATPASES THE
PERMEABILITY OF CELL MEMBRANES TO IONS, PARTICULARLY NA+ AND
INDIRECTLY CA2+, BECAUSE OF THE NA(+)-CA(2+)-EXCHANGE.
-I- SUBUNIT: MOMOMER AND HOMOTETRAMER (BY SIMILARITY).
                                                                                   Hemolysis;
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  Apis dorsata (Giant honeybee).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
Apoidea; Apidae; Apis.
NCBI_TaxID=7462;
                                                                                                                          ProDom;
                                                                                                                                     Pfam; PF01372; Melittin;
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HSSP; P01501; 2MLT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELITTIN.
                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                           The structure of Apis
                                                                                                                                                                                                                                                                                                                                                                               EQUENCE
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  243 RKRQE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGTES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-1-ANTI-CHYMOSTATIN, SOYBEAN TRYPSIN INHIBITOR,
PTM: EXTENSIVELY GLYCOSYLATED.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN
TRYPSIN FAMILY.
; S38295; S38295.
; P23346; IKIT.
pps: CA1 317
                                                                                                                                                                                                         DATABASE: NAME-Protein
                                                                                                                                                                                    WWW="http://www.expasy.org/spotlight/articles/sptlt012.html"
                                                                                                                                                                                                NOTE=Issue 12 of July 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00089; trypsin;
                         Similarity
5; Conser
                                                                                                                        PD014636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50240; TRYPSIN_DOM; PARTIAL PS00134; TRYPSIN_HIS; PARTIAL PS00135; TRYPSIN_SER; PARTIAL
                                                                                                                                               IPR002116; Melittin.
                                                                                                Toxin;
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001254; Trypsin.
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(Rel.
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                       1.8%;
ilarity 100.0%;
Conservative
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                                                                                    ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 01, Created)
. 01, Last sequ.
. 40, Last anno
                                                                                                Venom; Amidation
26 AMIDA
                                                                                                                        Melittin; 1
                                                                                     2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%;
100.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2822 MW;
                                                                                                                                                                                                                                                                                                                              is dorsata melittin: phylogenetic relationships
deduced from sequence data.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%;
                                                                                                                                                                                                         Spotlight;
                       Score 5; DB 1; Pred. No. 2.4 0; Mismatches
                          0;
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                                                                                   AMIDATION.
F1DA8F92514EF01C
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PARTIAL.
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                     DB 1; Leng
(0. 2.4e+02;
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                                              Length 26;
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RESULT 5
CPD1_ENTFA STANI
ID CPD1_ENTFA STANI
ID CPD2_ENTFA STANI
AC p13269;
DT 01-7AN-1990 (Rel. 1)
DT 01-FEB-1991 (Rel. 1)
DT 01-FEB-1991 (Rel. 1)
DE SEX PHEROMONE CPD1.
OS Enterococcus faecal
OC Enterococcus faecal
RM SECULINE=85040388; P.
RN MEDLINE=85040388; P.
RN MEDLINE=8504038; P.
RN MEDLINE=85040
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ECSI_HUMAN
ID EOSI_H
AC P02731
DT 21-JUL
DT 21
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   Query Match
Best Local S
Matches 4
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Best Local S
Matches 4
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VARIANT
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P02731;
P02731;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
21-JUL-1986 (Rel. 01, Last annotation)
EOSINOPHILOTACTIC PEPTIDES.
                                                                                                                                                                                                                                                                                    Science 226:849-850(1984).
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85040388; PubMed=Suzuki A., Mori M., Sagak Craig R.A., Clewell D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-i- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS (ANAPHYLAXIS). THETR ACTIVITIES, PREFERENTIALLY AFFECTING EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, REOF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=76078412; PubMed=1060093; Goetzl E.J., Austen K.F.;
                                                                                                                                                                                                                                                                                                                                                        "Isolation and structure of bacterial sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anaphylaxis.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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   Similarity 4; Conserv
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   ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                    PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=6436978;
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13, Last sequence up
17, Last annotation
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1.4%; Score 4; DB
100.0%; Pred. No. 1e-
ive 0; Mismatches
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Bacillus/Clostridium group; Enterococcaceae;
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/FTId=VAR_005201.
6B05B862A0000000 CRC64;
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                                                                                                                                                                                                                                                                                    THE CONJUGATIVE TRANSFER OF THE
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0. 1e+05;
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                                                                    Length 8;
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A LO COCCCCC REPORT FOR A REPOR
   Neuropeptide;
MOD_RES
MOD_RES
SEQUENCE 8 A
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PIR; S08995; S08995.
PIR; A49823; A49823.
PIR; A44960; A44960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaede G., Rinehart K.L. Jr.;

"Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the cardiaca of Periplaneta americana."; Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blatta orientalis (Oriental cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978, 7539, 6976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=B.orientalis; TISSUE=Corpora cardiaca; MEDLINE=90253659; PubMed=2340112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-B.orientalis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84298179; PubMed=6591205; Scarborough R.M., Jamieson G.C., Miller C.A., Schooley D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=P.americana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structures of two cockroach neuropeptides assigned bombardment mass spectrometry."; biochem. Biophys. Res. Commun. 124:350-358(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-P.americana;
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01-FEB-1994 (Rel. 28, Last annotation update)
HYPESTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994
01-FEB-1994
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13-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides 10:1287-1289(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The metabolic neuropeptides of the corpus cardiacum beetle and the American cockroach are identical.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90160053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rinehart K.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Witten J.L., Schaffer M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTF1_PERAM
                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85046530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eptinotarsa decemlineata (Colorado potato beetle),
                                                                                                                                                                                                                                                                                                                                                                               m bombardment mass spectrometry.";
1. Chem. Hoppe-Seyler 371:345-354(1990),
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the stick insect Extatosoma tiaratum assigned by tandem
                                                                                                                                                              PS00256; AKH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kellner R.;
                                                                                                                                                                                             IPR002047; AKH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel.
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(Rel.
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                                                                                                                  Amidation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neata; TISSUE=Corpora
PubMed=2576128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=6548628;
ffer M.H., O'Shea
       991 MW;
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PYRROLIDONE CARBOXYLIC ACID.
AMIDATION.
86745775B9C452D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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RESULT 8
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Best Local S
Matches 4
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Best Local
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                                                                                                                                                                                                                                                                                                                 OXYT_CYPCA
P23879;
                                                                                                                                                                                                                                               01-NOV-1991
01-NOV-1991
01-NOV-1995
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P25419;
01-MAY-1992
                                                                                                         Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Cyprinus. NCBI_TaxID=7962, 7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSAEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tenebrio.
SPECIES=C.carpio;
Acher R., Chauvet
"Characterization
                                                                      SEQUENCE.
                                                                                                                                                                                                                                 VASOTOCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuropeptide;
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR0020 PROSITE; PS00256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The primary structure of the hypertrehalosemic neuropeptide tenebrionid beetles: a novel member of the AKH/RPCH family.; peptides 11:455-459(190).
-i- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaede G., Rosinski G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=90341081; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7067,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 FSPN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 FSPN 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A43976;
B43976;
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PS00256; AKH; 1.
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TISSUE=Pituitary;
J., Chauvet M.-T., Crepy D.;
of neurohypophyseal hormones
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32,
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100.0%;
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100.0%;
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Last annotation update)
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Pred. No. 1et
0; Mismatches
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86745775B9C44736 CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC
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). 1e+05;
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    fresh water bony
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Best Local Similarity
Matches 4; Conserv
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_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-72215060; PubMed-5150741;
Chauvet J., Chauvet M.-T., Acher R.;
"Evolution of neurohypophyseal hormones:
principles from rabbits and rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit), Hippopotamus amphibius (Hippopotamus), Balaenoptera physalus (Finback Whale) (Common rorqual), Tachyglossus aculeatus aculeatus (Australian echidna), and Hydrolagus colliei (Spotted ratfish) (Pacific ratfish). Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
MOD_RES
SEQUENCE
SPECIES=A.aculeatus;
                          SEQUENCE
                                                                                                                 SPECIES=B.physalus;
Acher R., Chauvet J
                                                                                                                                                                                                                                 "Arginine and lysine vasopressins in the hippopotamus neurohypophysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXYTOCIN (OCYTOCIN).
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                                                                      Nature
                                                                                                                                                                                                                                                                                                     MEDLINE=71232719;
                                                                                                                                                                                                                                                                                                                               SPECIES-H.amphibius;
                                                                                                                                                                                                                                                                                                                                                                                                   Biochimie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=P.marinus; TISSUE=Pituitary; MEDLINE-88225976; PubMed=3371648; Lane T.F., Sower S.A., Kawauchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                 Ferguson D.R.,
                                                                                            "Isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Petromyzon marinus): isolation and amino Gen. Comp. Endocrinol. 70:152-157(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arginine vasotocin from the pituitary gland of the lamprey petromyzon marinus): isolation and amino acid sequence.";
                                                                                                                                                               EQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 QNCP 166
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SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNCP
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S06375; S06375.
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                                                                   tion of finback wha
201:191-192(1964).
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                                                                                       Chauvet J., Chauvet M.-T. of finback whale oxytoci
                                                                                                                                                                                                                                                                                                                                                                                                   53:1099-1104(1971).
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                                                                                                                                                                                                                                                                                                     PubMed=5406007;
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1053
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                                                                                                                                                                                                           13:425-429(1969)
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                                                                                                                                                                                                                                                                               B.T.;
                                                                                         oxytocin
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17EB176EB456D04B CRC64;
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Pred. No.
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Best Local Similarity
Matches 4; Conser
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OXYV_SQUAC
P43000;
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Hormone;
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                                                                                                                                                                                             Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
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PIR;
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                                                                                                             SEQUENCE
                                                                                                                             Acher R., Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial h
isolated from a cartilaginous fish,
Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                             01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oxytocin as a neurophyophysial hormone elasmobranch fish, Hydrolagus collei."; J. Endocrinol. 45:597-666(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature New Biol. 244:124-126(1973).
                          Pfam; PF00220;
                                                                                                                                                                                                                                    VALITOCIN.
                                                                                                                                                                                                                                                              01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=H.colliei;
MEDLINE=70088110; PubMed=5366118;
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"Neurohypophysial hormones and evol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=73223515; PubMed=4515919;
Acher R., Chauvet J., Chauvet M.
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; A93147; A93147.
; A93408; A93408.
; B90667; B90667.
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1XY2; 15-OCT-90.
rPro; IPR000981; Neurhypophys_horm.
               PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothalamus;
       Amidation.
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32, Last sequence 32, Last annotations.
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1010 MW;
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                                                                                                                                                                                                                                             sequence up
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17F8376EB456D04B CRC64;
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Best Local :
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P81758;

90-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 39, Last annotation update)

30-MAY-2000 (Rel. 39, Last annotation (PRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIC (EC 1.9.3.1) (FRAGMENT).
ONCOTHYNCHUS MYKISS (Rainbow trout) (Salmo gairdneri).
EUKATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostc.
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P80331;
01-OCT-1994
01-OCT-1994
                      Lopez de Felipe F.;
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of tissue-specific isoforms for cytochrome c oxidase isolated from rainbow Eur. J. Biochem. 221:1111-1116(1994)....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
MEDLINE=94237150; PubMed=8181469;
                                                                  STRAIN-IFPL731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED CHAINS OF CYTOCHOME C OXIDASE, THE TERMINAL OXIDAS MITOCHOMORIAL ELECTRON TRANSPORT.
-I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2
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                                                                                                                                NCBI_TaxID=1582;
                                                                                                                                                                              Bacteria; Firmicutes;
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SUBCELLULAR LOCATION: MITOCHONDRIAL
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P80243;
01-FEB-1995
01-FEB-1995
20-AUG-2001
                                                                                                                                                                                                                                                           TRP5_LEUMA STANDARD; PRT; 10 P
9811973;
90-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update
30-MAY-2000 (Rel. 39, Last annotation update
TACHYKININ-RELATED REPTIDE 5 (LEMTRP 5).
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SEQUENCE
        Muren J.E., Naessel D.R.;
Muren J.E., Naessel D.R.;
"Isolation of five tachykinin-related peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 140:741-752(1994).
-!- INDUCTION: BY HEAT SHOCK, SALT STRESS,
LIMITATION AND OXYGEN LIMITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/
Bacillus/Staphylococcus group;
NCBI_TaxID=1423;
the cockroach isoforms.";
                                                                             TISSUE=Midgut;
MEDLINE=97053012; PubMed=8897641;
                                                                                                                                                                                  Pterygota; Ne
Blaberoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of the induction of subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Voelker U., Engelmann S., Maul
Schmid R., Mach H., Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YZZF
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                                                                                                                                                                                                                          Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94282319; PubMed=8012595;
Voelker U., Engelmann S., Maul B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-IS58
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                                                                                                                      SEQUENCE
                                                                                                                                                          NCBI_TaxID=6988;
                                                                                                                                                                                                                        Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat shock; Complete
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                                                                                                                                                                                                   Neoptera; Orthopteroidea; Dictyoptera;
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
ESS PROTEIN 9 (GSP9) (FRAGMENT).
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0; Mismatches
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Pred. No.
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Regul. Pept. 65:185-196(1996). [2]

SEQUENCE, AND MASS SPECTROMETRY.

TISSUE=Brain;

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LPW_THETH
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN+HB8 / ATCC 27634;
MEDLINE-89000781; Pubmed-2844259;
MEDLINE-89000781; Pubmed-284259;
Sato S., Nakada Y., Kanaya S., Tanaka T.;
"Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and trpG.";
Biochim. Biophys. Acta 950:303-312(1988).
-i- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPW_THETH STANDARD; PRT; 11 AA. P05624; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) TRP OPERON LEADER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
-i- TISSUE SPECIFICITY: MUIGOT AND BRAIN.
-i- MASS SPECTROMETRY: MW=1033.2; METHOD-MALDI.
-i- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
Tachykinin; Neuropeptide; Amidation.
MOD_RES 10 10 10 AMIDATION.
SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769D CRC64;
                                                                                                                                                EMBL; x07744; CAA30565.1; -.
PIR; S03315; LFTWWE.
Tryptophan biosynthesis; Leader peptide.
SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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|||||
2 PAMG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus aquaticus (subsp. thermophilus).

Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides 18:7-15(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muren J.E., Naessel D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97269266; PubMed=9114447;
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                                38 ALPS 41
 N
ALPS 5
                                                                   Conservative
                                                                1.4%; Score 4; DB 1; Le 100.0%; Pred. No. 1.2e+03; Live 0; Mismatches 0;
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Search completed: January 24, 2002, 16:29:16 Job time: 191 sec

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Perfect score:
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Copyright (c) 1993 - 2000
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P82671
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Q9T2I9
Q9T2I8
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Q9R4I3
Q9NQR3
Q9UIH1
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P82671 spinacia ol
O9r5b9 aeromonas s
O9t2i9 nicotiana s
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O52266 bacillus th
O94374 caenorhabdi
O9r4b4 aeromonas t
O14497 homo sapien
O9n0z9 sus scrofa
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09t2i8 nicotiana:
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052266 bacillus t:
094374 caenorhabd:
09r4b4 aeromonas:
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09n0z9 sus scrofa
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071988 human immu
071988 human immu
09sge5 vicia fabbi
09sin7 arabidops
Q9nqr3
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Q9fux5 symphoricar
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Q9q2n4 chlamydosau			-		Q9g5v6 phrynocepha	Q9g5v9 laudakia st	_	trapelus	Q9g5x4 trapelus ag			Q9g673 ctenophorus	079985 laudakia ca	•		Q16217 homo sapien	Q85619 moloney mur	_	Q99213 aegilops sq	P82384 drosophila	Q9tlm7 laurencia v	Q9tuy0 monodelphis	Q9yiq9 human adeno	Q9yir0 human adeno	Q9yve3 human adeno

## ALIGNMENTS

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Query Match
Best Local S
Matches 5
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Q9R5T6;
01-MAY-2000
01-MAY-2000
01-MAY-2000
O9FUX5 PRELIMINARY; PRT; 14 AA.
O9FUX5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MAXY (FRAGMENT).
Symphoricarpos albus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                           MEDLINE=91372953; PubMed=1680105; Hokama A., Iwanaga M.; Purification and characterization of Aeromonas sobressible colonization factor."; Infect. Immun. 59:3478-3483(1991). SEQUENCE 10 AA; 1143 MW; 4C19F942C72B1057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aeromonas sobria.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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0; Mismatches
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MEDLINE=96090101; PubMed=7581267;
Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
"Immunoaffinity chromatographic isolation of a high molecular weight seroreactive protein from Mycobacterium leprae cell sonicate.";
FEMS Immunol. Med. Microbiol. 11:163-169(1995).
SEQUENCE 16 AA; 1842 MW; 54A9ECCA5044F83E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harv. Pap
EMBL; AF2
NON_TER
SEQUENCE
   SEQUENCE
                     "Characterization of Aeromonas sobria TAP13 pili: a colonization factor.";
                                                                                                                                01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                               Q9R5G4;
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Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID-1769;
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01-MAY-2000 (TremBLrel.
01-MAY-2000 (TremBLrel.
MLP SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DylJogeny and biogeography of Thlarv. Pap. Bot. 5:157-166(2000).
EMBL; AF277633; AAG31453.1; -
NON_TER 1
                                                  MEDLINE=93018994; PubMed=1357078
                                                                                                     Bacteria;
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                                          Iwanaga M., Hokama
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NCBI_TaxID=13702;
                                                                                NCBI_TaxID=646;
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Last sequence update)
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 60A8BF885E6B236C CRC64;
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Chloroplast; Thylakoid membrane.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
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Submitted (MAY-2000) to the SWISS-PROT data
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14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Aeromonadaceae;
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                                                                                                                 Score 5; DB 2; Pred. No. let 0; Mismatches
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Pred. No. 8.8
0; Mismatches
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Pred. No.
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. le+03;
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09T2I8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
14.1 KDA PHOTOSYSTEM I PSAE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obokata J., Mikami K., Hayashida N., Nakamura "Molecular heterogeneity of photosystem I. psa psat are all present in isoforms in Nicotiana Plant Physiol. 102:1259-1267(1993).
SEQUENCE 20 AA; 1822 MW; E458944E2F5E5D94
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SEQUENCE 20 AA; 1822 MW; A89458943928ZE5D CRC6
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01-MAY-2000 (TREMBLIEL 13, Last sequence update)
01-JUN-2000 (TREMBLIEL 14, Last annotation update)
14 KDA PHOTOSYSTEM I PSAE PROTEIN (FRAGMENT).
NICOLIANA SYLVESTIS (Wood tobacco).
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Q9R4B4 PRELIMINARY;
Q9R4B4;
01-MAY-2000 (TrEMBLrel. 13,
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Q94374;
Q94374;
Q1-FEB-1997 (TrEMBLrel. 02, Created)
O1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PP1-LIKE SER/THR PROTEIN PHOSPHATASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-90253151; PubMed-2160219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FRAGMENT).
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Iron; Manganese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00149; STphosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pBC16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000934; Ser_thr_phosphtse
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                                                                                                                                                                DVLRL
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5; Conservative
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Pred, No. 1.0
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D. 1.1e+03
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Matches 5
     Q9N0Z9 PRELIMINARY; PRT; 25 AA.
Q9N0Z9;
Q9N0Z9;
101-OCT-2000 (TrEMBLrel. 15, Created)
101-OCT-2000 (TrEMBLrel. 15, Last sequence update)
101-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ARYLHYDROCARBON RECEPTOR (FRAGMENT).
Sus scrofa (Pig).
EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; EuMammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Su NCBL_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                              Q14497 PRELIMINARY; PRT; 25 AA. Q14497; 01-NOV-1996 (TrembLrel. 01, Created) 01-NOV-1996 (TrembLrel. 01, Last sequence update) 01-NOV-1996 (TrembLrel. 01, Last annotation update) 01-NOV-1996 (TrembLrel. 01, Created) 01-NOV-1996 (TrembLrel. 01, Cast annotation update) 01-NOV-1996 (TrembLrel. 01, Cast annotation update)
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Microbiology 142:309-313(1996).
SEQUENCE 25 AA; 2697 MW; BFCABF6292AA889
                                                                                                                                                                                                                                                                                     EMBL; 270024; CAA93846.1; NON_TER 25 25
                                                                                                                                                                                                                                                                                                Submitted (MAR-1996) to the EMBL/GenBank/DDBJ EMBL; 270024; CAA93846.1; -.
                                                                                                                                                                                                                                                                                                                            TISUE=BRAIN;
Dmitrenko V.V., Garifulin O.M.,
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                           SEQUENCE
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01-MAY-2000
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Nakasone N., Iwanaga M., Yamashiro T.,
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nilarity 100.0%;
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Q71988
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C)71988;
C)71996 (TrembLrel. 01, Cr
T 01-NOV-1996 (TrembLrel. 11, Lr
JT 01-JUN-2001 (TrembLrel. 17, L
DATIENT 3799(12-88), CLONE 3?
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=PATIENT 3799(12-88);
MEDLINE=95287475; PubMed=7769682;
Michael N.L., Chang G., d'Arcy L./
                                                                                                                                        Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00424; REV;
NON_TER 25
SEQUENCE 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arch. Virol. 145:1021-1027(2000).
EMBL; AB034363; BAA93826.1; -.
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EMBL; AF233432; AAF43428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada T., Iwamoto A.;
"Comparison of proviral accessory
nonprogressors and progressors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REV
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Ehrenberg

P.K.,

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RA Busch M.P., Birx D.L., Schwartz D.H.;
RT "Defective accessory genes in a human immunodeficiency virus type 1-
RT infected long-term survivor lacking recoverable virus.";
RL J. Virol. 69:4228-4236(1995).
RR EMBL; U24481; AAA79642.1; -.
DR InterPro; IPR000625; REV.
DR InterPro; IPR000625; REV.
DR INCEPPO 124; REV; 1.
FT NON_TER 25
S0 SEQUENCE 25 AA; 2744 MW; 1F922F59A5DF261D CRC64;

Query Match
Best Local Similarity 100.0%; Score 5; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 218 TWGLI 222
[111]
Db 15 TWGLI 19

Search completed: January 24, 2002, 16:29:00
Job time: 190 sec
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Result
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			/Qualifiers sig_peptide mat_peptide		rr necrosis factor; TNF; receptor; trinhibition; identification; agonist; T cell; differentiation; mediation; response; regulation; growth; protect hlamydia; infection; immunodeficiencisease; inflammation; septic shock; cell; cancer; graft; host; reaction; apoptosis; cytotoxicity; hybridisatintibody; reagent.	receptor.		•	283 AA.	ALIGNMENTS	AAY54443 AAB37685 AAY94718	AAW89234 AAY54441	AAW52270	AAY//463 AAB66981	AAR77421	AAR2/803 AAR85071	AAB66980	AAB84892 AAB50520	AAR38859 AAY52701	AAY32191 AAY33499	AAY95322 AAY94715	AAY94719 AAW05811	AAW05810	AAW60046	AAY79205 AAY79206	AAY79207 AAY79204	AAY05797
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					ment; tagonist; mune; ; HIV; virus; ebral; malaria; jection; probe;						Wild type N-termna Human 40 kDa TNF i Human type 2 tumou	necros	Tumour necrosis fa	ce prote protein	BamTP delta53 nerv	Shope fibroma viru	Human CD40. Homo Sfu-t2 protein. U	Human CD40 antigen Human tumour necro	CD40 protein. Hom Human CD40 protein	CD40 protein. Uni Human CD40 protein	Pig costimulatory Murine CD40 protei	Human TR2-receptor Human tumour necro	Human tumour necro		herpesvir herpesvir	ne-bour e herpe	Herpes virus entry

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     Homo sapiens
                                                                                        Entry mediator gene; herpesvirus; HVEM; tumour necrosis 1
gene expression regulator; cellular stress; inflammatory
                                                                                                                                                                                Herpesvirus
                                                                                                                                                                                                                                     21-OCT-1998
                                                                                                                                                                                                                                                                                                                                                  AAW69238 standard; Protein;
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                                                                                                                                                                             entry mediator protein
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                                                             regulator; autoimmune response.
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Pred. No. 4.5
0; Mismatches
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4.5e-121;
                                                                                                                  tumour necrosis factor receptor;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription factors, e.g. AP-1, suggesting that HVEM is involved in regulating gene expression in response to infectious stimuli and cellular stress. The predominant expression of HVEM mRNA in lymphocyte-rich tissues (e.g. spleen and peripheral blood) also suggested it may be a receptor in regulating lymphocyte activity. Antibodies produced may therefore be useful therapeutically, e.g. antagonistic antibodies may be useful to block excessive inflammatory/autoimmune response resulting from e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM regulation of such induction. The DNA may be used diagnostically, e.g. to determine if DNA and/or RNA encoding HVEM is present in cells, and to prepare HVEM polypeptide recombinantly. It is also useful to produce non-human transgenic animals (e.g. mice or rats), especially knockout such animals are useful in the development and screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention. The protein is useful in quantitative diagnostic assays for HVEM, in affinity purification of HVEM from recombinant cells/natural sources and in competitive-type receptor binding assays. It can also be used to generate antibodies, also useful in diagnostic assays for HVEM and affinity purification of HVEM, HVEM is believed to be a member of the tumour necrosis factor receptor (TNFR) family, and transient transfection of HVEM into human 293 cells caused marked activation of certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in assays for HVEM and to produce antibodies and transgenic animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the herpesvirus entry mediator (HVEM) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1996;
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                                                                                                                                                                                                                                                                                             1 MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
                                                   HQTKCSWLYTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                                                                                                                 CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                         YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                          \verb|cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq|\\
                                                                                                                                                                                                   yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                                                                                                                                                            meppgdwgpppwrstprtdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg
                                                                                                                                               283;
                                                                                                                                                                                                                      Conservative
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Pred. No. 4.5e-121;
); Mismatches 0;
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RESULT AAYOGABA ID WAYO AX AAYO AY AAYO AAYO
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                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 283; Conservative 0
                                                                                                                                                                                                                                                                                                                                     This sequence represents human PRO509 (UNQ329), a protein encoded by the novel cDNA clone DNA50148 (see AAX87264), and a member of the tumour necrosis factor receptor family. Amplification of DNA50148 was observed in various tumour tissues, suggesting a role in tumour formation or growth. Antagonists (e.g. antibodies) directed to PRO509 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX66477-90) may be useful targets for the diagnossis and/or treatment (including prevention) of certain cancers.
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10-JUN-1998;
10-NOV-1998;
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05-JAN-1998;
29-APR-1998;
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                     and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claim cancer diagnostic kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody against proteins expressed tumor diagnosis and treatment
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98US-0107783.
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98US-0070440.
98US-0083500.
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201..225
/note= "transmembrane domain"
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                                                                                                Score 1578; DB 20;
Pred. No. 4.5e-121;
; Mismatches 0;
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RESULT
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26-MAR-1999;
20-MAY-1999;
06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                    Nucleic acid molecule encoding a human tumor necrosis factor receptor and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and
                                                                                                                                                               (NIJJ/)
(ROSE/)
                                                           and its two splice variants, useful for tinflammation, cancer (such as follicular immunodeficiency disorders -
                                                                                                          N-PSDB;
                                                                                                                                    Ni J,
                                                                                                                                                                                                                                                                                                      Protein
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DB; AAA28149.
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                                                                                                                                    Rosen CA,
                                                                                                                                                    NI J.
ROSEN
GENTZ
                                           Page 370;
                                                                                                                                                                                                                                      2000WO-US07521
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99US-0126522.
99US-0135169.
99US-0147383.
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39..283
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                                                                                                                                    Gentz
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                                          373pp;
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                                           English.
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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2 The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

p36.2-p36.3.

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC antiniflammatory, neuroprotective, noctropic, antiparkinsonian, and CC cerebroprotective activity. The methods are useful for treating arthritis CC or inflammatory, cancer (such as follicular lymphomas, carcinoma with p53 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an cc antigen. Anti-TR2 antibodies are useful for treating, inhibiting or CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia, CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and CC inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency (SCID)-x linked, B cell lymphoprolliferative CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2, CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, cc cancerous for generating antibodies, as molecular weight markers.

CC This sequence represents the TR2 receptor protein of the invention.
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Best Local
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                                                                                 Homo sapiens
                                                                                                                                        PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
                                                                                                                                                                                                                                            03-OCT-2000
                                                                                                                                                                                                                                                                                                                       AAY93695 standard; Protein; 283
                    Peptide
                                                                                                                    tumourigenesis; cancer; neoplastic cell growth;
                                                                                                                                                                                               Amino acid sequence of novel polypeptide PRO509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a fragment of the TR2 protein. TR2 its agonists, antagonists and antibodies exhibit cytostatic, dermatological, antianaemic, immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           member of the TNFR superfamily. The invention includes a
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                                                                                                                                                                                                                                                                                                                                                                                                                     vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh 283
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/note= "signal sequence"
                                        Location/Qualifiers
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Query Match
Best Local Similarity
Matches 283; Conserv

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Score 1578; DB 21; Pred. No. 4.5e-121; ; Mismatches 0;

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08-MAR-1999;
02-JUN-1999;
                             The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the prognosis of tumour centent. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
Sequence
                                                                                                                                          Claim 61; Fig
                                                                                                                                                                                               WPI; 2000-452188/39.
N-PSDB; AAA46931.
                                                                                                                                                                                                                              Wood
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                     proliferation in
 283 AA;
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                                                                                                                                        24; 220pp; English
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99WO-US05028.
99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28313.
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99WO-US28301.
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173..177
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120..126
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110..114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cell attachment sequence"
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                                                                                                                                                                                                                                                             PRO509; human; antitumour; tumour; therapy; cytostatic; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm.
       02-DEC-1999;
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                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                              Human PRO509 antitumour protein.
                                                                                                                                                                                                                                                                                                                         AAY95348
                                                                                                                                                                                                                                                                                                                                      AAY95348 standard; Protein;
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       99WO-US28565
                                                   /note= "
231..234
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173..177
                                                                                                                                  /note= "/
153..159
                                                                                                                                              /note= "r
120..126
                                                                                                       /note= "
192..201
                                                                                                                     /note=
193..1
                                                                                                                                                                        /note= "N-myristoylation" 89..95
                                                                                                                                                                                                                /label= Signal_peptide 37..283
                                                                                                                                                                                             205..221
/note= "transmembrane domain"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                  /note=
                                                                                                                                                                  note= "N-myristoylation"
                                                                                                                                                                                                          /label= PRO509
                                                                                    note=
                                                                                                                     ..199
                                                                      "Asn
                                                         "Asn is N-glycosylated"
                                                                                    "N-myristoylation"
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                                                                                                                                                     "N-myristoylation"
                                            "cell attachment sequence"
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Best Local
                  AAW60045 standard;
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22-DEC-1998

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21-APR-1999

28-APR-1999

14-MAY-1999

20-JUL-1999

26-JUL-1999

15-SEP-1999

15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of human antitumour protein PRO509, as deduced from a retinal cDNA clone (see AAA49727). PRO509 shows homology to members of the human tumour necrosis factor receptor family such as the lymphotoxin-beta receptor (11 identities) and CD40 (12 identities). A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO221, PRO2256, PRO326, PRO326, PRO326, PRO326, PRO326, PRO327, PRO327, PRO327, PRO327, PRO327, PRO336, PRO509 or PRO866 (see AAY95337-49), their agonists chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant expression of the antitumour proteins are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition to inhibit neoplastic cell growth or for treetumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO221, PRO324, PRO308, PRO301, PRO526, PRO362, PRO366, PRO509
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N-PSDB; AAA49727.
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                   241 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                                              / Match 100.0%;
Local Similarity 100.0%;
nes 283; Conservative (
                                                                                                                                                                                                                                               CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh
                                                                                                                                                              cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
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99WO-US21090.
99WO-US21547.
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99WO-US05028.
99US-0130232.
99US-0131445.
99US-0134287.
99US-0144758.
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Pred. No. 4.5e-1
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Protein;

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25-SEP-1998

(first

entry)

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Query Match
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                                                                                                                                         Matches
                                                                                                                                                                                                                                                    The human tumour necrosis factor (TNF) receptor related protein (TR2) is a member of the TNF family and displays considerable homology to murine CD40. It can be used in soluble forms to treat herpes simplex virus infection and TR2 proteins (or their agonists or antagonists) are used to treat disease associated with aberrant cell survival. Agonists may also be used to protect against the effects of radiation therapy and to stimulate lymphocyte proliferation and differentiation in patients infected by human immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding TR2 tumour necrosis factor family receptor and its splice variants, useful for diagnosis and treatment of diseases involving abnormal cell survival or death, e.g. herpes simplex infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-)
                                                                                                                                                                                                                             Sequence
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                YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
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SMITHKLINE BEECHAM CO
                                                                                                                                                         Similarity
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                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               necrosis factor; TNF; herpes
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173
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110
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37..20
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                                                                                                                                       Score 1575; DB 1
Pred. No. 8e-121;
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Query Match Best Local S Matches

Similarity

99.8%;

Score 1575; DB 2 Pred. No. 8e-121; Mismatches

20; 0;

Length Indels

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                                        This sequence represents the human tumour necrosis factor (TNF) receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can be used in the method of the invention to treat pathological conditions. The method is used to treat systemic lupus erythematosus, idiopathic thrombocytopaenic purpura, rheumatoid arthritis, multiple sclerosis, psoriasis, inflammatory bowel disease, insulin-dependent diabetes mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic dermatitis, cancer, e.g. lymphomas and leukaemias, artherosclerosis and viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody is also used to monitor and diagnose abnormalities in TR-2 function,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis; systemic lupus erythematosus; idiopathic thrombocytopaenic purpura; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease; insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;
                              production
                                                                                                                                                                                                                  Disclosure; Page 27-28; 35pp; English.
                                                                                                                                                                                                                                                Method of treating pathological condition - tumour necrosis factor-2 antibody to patient
                                                                                                                                                                                                                                                                                               WPI; 1999-059689/05
N-PSDB; AAV83763.
                                                                                                                                                                                                                                                                                                                                            Harrop JA,
                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artherosclerosis; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour necrosis factor receptor-like 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-1999
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                             or metabolism.
283
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                                                                                                                                              22-MAR-1999;
26-MAR-1999;
20-MAY-1999;
                                                                                                        (NIJJ/)
(ROSE/)
                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
       Nucleic acid molecule encoding a human tumor necrosis factor and its two splice variants, useful for treating arthritis inflammation, cancer (such as follicular lymphomas) and
                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                            Domain
                                                                             Ni J,
                                                                                                                                      06-AUG-1999;
                                                                                                                                                                                    22-MAR-2000;
                                                                                                                                                                                                      28-SEP-2000.
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                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TR2-receptor protein sequence
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                                                                                              (GENT/)
immunodeficiency disorders
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                                                                            Rosen CA,
                                                                                              NI J.
ROSEN
GENTZ
                                                 AAA28135
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                                                                                                                                     99US-0125683.
99US-0126522.
99US-0135169.
99US-0147383.
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                                                                                                                                                                                                                                                      /note=
226..2
                                                                                                                                                                                                                                                                                           /label= "TR2 receptor" 37..200
                                                                                                                                                                                                                                                                                                              /note= "Signal peptide" 37..283
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                                                                             Gentz
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XX XX Claim 1; Fig 1; 373pp; English.

XX This invention relates to an isolated nucleic acid molecule encoding a CC human tumour necrosis factor(TNF)-receptor related protein TR2. Included CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2. CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a CC member of the TNPR superfamily. The invention includes a method for the CC treatment of arthritis or inflammation using an antibody directed against C antibodies exhibit cytostatic, dermatological, antiansamic, C antionists and c cerebroprotective, antiallergic, antiarthritic, antiasthmatic, antiations, cancer (such as follicular lymphomas, carcinoma with p53 c mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukcoyte response to an immunodeficiency or for enhancing an in vivo leukcoyte response to an c mingen. Anti-TR2 antibodies are useful for treating, inhibiting or c preventing autoimmune diseases (such as autoimmune haemolytic anaemia, and C inflammatory myopathies) and immunodeficiency disorders (such as secondars) as autoimmune haemolytic anaemia, and c inflammatory myopathies) and immunodeficiency with 1gs) TR2. C TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or c antagonists are useful for treating or preventing autoimmune diseases and c inhibit the growth, progression and/or metastasis of cancers. They are C inhibit the growth, progression and/or metastasis of cancers. They are C anseomists are used to treat diseases associated with increased cell c survival, or the inhibition of apoptosis, e.g. Alzheimer's disease, and c clisues, and can be used to treat diseases as and inhibit markers.

C This sequence represents the TR2 receptor protein of the invention.
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Query Match Best Local Matches 181 181 121 121 61 61 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG  $\verb|vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh|$  ${\tt cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq}$ meppgdwgpppwrstpktdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg Similarity Conservative 99.8%; 99.6%; Score 1575; DB 21; Pred. No. 8e-121; Mismatches 0; 283 283 Indels Length 0; Gaps 180 120 120 240 240 180 60 60 0

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AAW95031

AAW95031

standard; protein;

13-MAY-1999

(first entry)

Tumour necrosis factor receptor (TNF-R) related polypeptide

Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2;

inflammation; septicemia; autoimmune disease;

transplant rejection;

TL4;

TR2.

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В
                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNN-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, athersclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide TR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1997;
13-AUG-1997;
26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome;, restenosis, bone disease; cancer; athersclerosis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) useful for treating stroke, Alzheimer's disease and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13-14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brigham-burke MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1998;
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nes 282; Conserv
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                 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                             HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                             cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
                                                                                                                                                             CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                                                                                                                                                                                            MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
vqrkrqeaegeatviealqappdvttvaveetipsftgrspnh
                                                                                                                                                                                                                               YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                   283 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
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97US-0055513.
97US-0056980.
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                                                                                                                                                                                                                                                                                                                                              99.6%;
                                                                                                                                                                                                                                                                                                                                              Score 1572; DB 20;
Pred. No. 1.4e-120;
                                                                                                                                                                                                                                                                                                                                Mismatches
 283
                                                                                                                                                                                                                                                                                                                                                               Length 283;
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AAW12659 RESULT δÃ

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Human herpes simplex virus (HSV) cellular mediator (HVEM) (AAW12659) is a novel member of the TNF/MGF receptor family that mediates or enhances entry of HSV into cells. Its amino acid sequence was deduced from a cDNA clone (AAT51737) isolated from an HeLa library by its ability to convert CHO-KI cells from resistance to susceptibility to HSV-1 entry. Recombinant HVEM can be produced in bacterial or mammalian (esp. CHO) cells. It can be used as an immunoassay reagent to detect specific antibodies, to screen for
                                                                                                                                                                                                       New human herpes simplex virus cellular mediator - used for diagnosis, drug screening and therapeutically to inhibit entry HSV into cells
                      drugs having an (ant)agonist effect on HSV entry into cells, generate antibodies, to screen for the (currently unknown) H ligand, and to identify inhibitors of HSV-HVEM interaction.
                                                                                                                                                                             Claim 1; Fig 2; 54pp;
                                                                                                                                                                                                                                                       WPI; 1997-145273/13.
N-PSDB; AAT51737.
                                                                                                                                                                                                                                                                                               Montgomery RI,
                                                                                                                                                                                                                                                                                                                       (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                              WO9704658-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; agonist; antagonist; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human herpes simplex virus cellular mediator
                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW12659 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                  95US-0509024.
                                                                                                                                                                                                                                                                                                                                                                           96WO-US12374.
                                                                                                                                                                                                                                                                                               Spear PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Label= 1
110..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Glycosylation
/note= "potential N-glycosylation site"
173..175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "cysteine-rich repeat characteristic
TNF/NGF receptor family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mat_protein
42..75
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "partial cysteine-rich repeat characteristic
  of TNF/NGF receptor family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cysteine-rich repeat characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cysteine-rich repeat characteristic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283
                                                                                                                                                     cellular mediator (HVEM) (AAW12659)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family"
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Indels Length

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283; 0,:

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Query Match
Best Local
         virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 (see AAV05796) and/or HVEM receptor proteins enables the development of assays for screening antiviral compounds and therapeutics. The assays are useful for detecting the ability of agents to inhibit HSV entry or spread and provide for facile high-throughput screening of compounds suspected to be able to inhibit such entry,
                                                                                                                                                 The present sequence represents HVEM, a novel human herpes simplex
                                                                                                                                                                          Claim 10; Page 71-72; 89pp; English.
                                                                                                                                                                                                      Human herpes simplex virus
                                                                                                                                                                                                                                                WPI; 1999-302740/25.
                                                                                                                                                                                                                                                                          Fuller AO,
                                                                                                                                                                                                                                                                                                   (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                              22-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                    simplex virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry mediator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
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99.3%;
peptide libraries etc.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HVEM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiviral; assay
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Pred. No. 2e-120;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                        Subramanian
                                                                                                                                                                                                       HVEM
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Best Local
                                                                                                                                                                                                                                                                                                                                                                              mHVEM-2; membrane-bound herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; herpes simplex virus; infection; cancer; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potential drug candidates. Comprising the HSV receptor, fragments of the polypeptide
16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY79207 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                          WO200014230-A1
                                                                  Modified-site
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                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  autoimmune disorder; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane-bound herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY79207
                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cspghfcivqdgdhcaacrryatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglratrncsrtenavcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                           /note= "
                                                                                                                                                                                                                                                                       /note=
39..277
                                                                /note= "N-glycosylated"
                                                                                            110
                                                                                                                      /note=
201..2
                                                                                                                                                 165.
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                                                     /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                 ..186
                                                                                                                       . 225
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                                                                                                                                                                                                                "cysteine-rich domain"
                                                                                                                                                                                       "cysteine-rich domain"
                                                                                                                                                                                                                                                                                   "signal peptide"
                                                    "N-glycosylated"
                                                                                                      "transmembrane domain"
                                                                                                                                 "cysteine-rich domain (partial)"
                                                                                                                                                            "cysteine-rich domain"
                                                                                                                                                                                                                                            "mature protein, also separately claimed in Claim \mathbf{8}\text{ }^{\text{n}}
                                                                                                                                                                                                                                                                                                                                                                                                                                    entry mediator-2 (mHVEM2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1570;
Pred. No. 2e
1; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention also provides , an immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2e-120;
                                                                                                                                                                                                                                                                                                                                                                                inflammation;
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human;

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XX Herp
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XX Huma
XX Huma
XX 22-C
XX 22-C
XX 22-C
XX WPI;
PR 22-C
XX WPI;
PR 1011
XX WP

N-PSDB;

03-SEP-1999;

99WO-US20180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C (see AAZ94198). mHYEMZ is a TANGO-69-receptor and member of the C tumour necrosis factor receptor (PNPR) superfamily. HYEM plays a crole in herpes simplex virus (HSV) entry. The invention is based to the discovery of 3 cDNA molecules (see AAZ94195-97) which encode c soluble forms (see AAZ9204-66) of mHYEM, and the cDNA molecule c encoding of mHYEMZ. In addition to isolated full-length proteins c and polynucleotides, and invention provides TANGO-69-receptor c ission proteins, antigenic peptides and antibodies. Also provided c are recombinant expression vectors, host cells and transgenic c animals in which a TANGO-69-receptor gene has been introduced or c disrupted. DNA encoding HYEM, HYEM proteins and HYEM antibodies c can be used in screening and detection assays (e.g., chromosomal c mapping, tissue typing). HYEM proteins can also be used for regulation of cell proliferation, cell activity, HSV infection and/or c regulation, and/or coagulation. HYEM agonists can be used to treat disorders associated with decreased HYEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Matches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammat allergic inflammation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel form of membrane-bound herpesvirus entry mediator (mHYEM). The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94198). mHYEM2 is a TANGO-69-receptor and member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide, the mature portion of which is also claimed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Busfield SJ
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29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM BIOTHERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is human membrane-bound herpesvirus entronovel form of membrane-bound herpesvirus
                                                                                                                                                                                                       121
                                                                               181
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                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                             MEPPGDWGPPPWRSTPRTDVLRLYLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
                                                                                                                                                                                CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                                                                                                                                                                                                                                                               YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
vq-----vlillplslpp
                                       VQRKRQEAEGEATVIEALQAPP 262
                                                                           yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                                                                                                                                                                                                        meppgdwgpppwrstprtdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-256981/22.
)B; AAZ94198.
                                                                                                                       HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
                                                                                                                                                           cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 7; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0146950
99US-0342767
                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%;
93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herpesvirus entry mediator-2 (mHVEM2), a
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1373.5; DB 21; Pred. No. 2.1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               277;
                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 14
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(See AAZ94195). SHYEMI is a TANGO-59-receptor and member of the thought to play a role analagous to other soluble members of the TWFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 CDNA molecules (see AAZ94195-97) which encode soluble forms (see AAY79204-06), and I cDNA molecule (see AAZ94198) that encodes a 2nd membrane-bound form (see AAY9207), of mHVEM. In addition to isolated full-length proteins and polynucleotides, and Invention consolites TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, host cells and transgenic animals in which a TANGO-69-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays - \,
                                                                                                                                                                                                                                                                                              This polypeptide, the mature portion of which is also claimed, is human soluble herpesvirus entry mediator-1 (sHVEM1), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-256981/22.
N-PSDB; AAZ94195.
                                                                                                                                                                                                                                                        The amino acid sequence was deduced from an isolated cDNA clone (see AAZ94195). SHVEM1 is a TANGO-69-receptor and member of the
                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Fig 1; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1998;
29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHVEM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble herpesvirus entry mediator-1 (sHVEM1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200014230-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soluble herpesvirus entry mediator-1; TANGO-69-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0146950.
99US-0342767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US20180
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110
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37..19
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er; inflammation; autoimmune disorder; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= ."N-glycosylated"
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "c
121..162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "mature protein, also separately claimed in Claim 8\,{}^{\rm m}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                   (mHVEM).
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RRESULT 1
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KW SHVE
KW CLUMO
KW CALM
XX SHVE
KW CALM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sHVEM-2; soluble herpesvirus entry mediator-2; TANGO-69-receptor; tumour necrosis factor receptor; human; herpes simplex virus; infection; cancer; inflammation; autoimmune disorder; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders.
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     16-MAR-2000
                                                     WO200014230-A1
                                                                                                                               Modified-site
                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQTKCSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herpesvirus entry mediator-2 (SHVEM2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AA;
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                                                                                                                                                                                                                                                                                  /note= '78..119
                                                                                                                                                                               /note=
110
                                                                                                                                                                                                                               /note= "c
121..162
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "signal peptide"
39..197
                                                                                                                               /note= "N-glycosylated"
173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                  "N-glycosylated"
                                                                                                                                                                                                                                                                                                          "cysteine-rich domain"
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                                                                                                                                                                                                       "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                            "mature protein, also separately claimed
in Claim 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1068; DB 21; Length Pred. No. 1.2e-79; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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(see AAA94196). SHVEM2 is a TANGO-69-receptor and member of the tumour necrosis factor receptor (PNFR) superfamily. It is thought to play a role analagous to other soluble members of the TWFR superfamily by interfering with the ability of LIGHT-TANGO-69 and lymphotoxin to bind mHVEM, and to play a role in herpes simplex virus (HSV) entry. The invention is based on the discovery of 3 C cDNA molecules (see AAA94195-97) which encode soluble forms (see AAY9204-06), and 1 cDNA molecule (see AAZ94198) that encodes a 2nd membrane-bound form (see AAY9207), of mHVEM. In addition to isolated full-length proteins and polynuclectides, and invention provides TANGO-69-receptor fusion proteins, antigenic peptides and antibodies. Also provided are recombinant expression vectors, bast cells and transgenic animals in which a TANGO-69-receptor gene has been introduced or disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing). HVEM proteins can also be used for regulation of cell proliferation, cell activity, inflammation mast cell activity,
                                     HSV infection and/or proliferation, and/or coagulation. HVEM agonists can be used to treat disorders associated with decreased HVEM activity, e.g. proliferative disorders such as carcinoma or pathogenic infection. Antagonists can be used to treat disorders associated with increased HVEM activity, e.g. autoimmune, T cell, inflammatory and allergic inflammation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening assays and detection assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is human soluble herpesvirus entry mediator-2 (sHVEM2), a novel soluble form of membrane-bound herpesvirus entry mediator (mHVEI The amino acid sequence was deduced from an isolated cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide, the mature portion of which is also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 3; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Busfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1998;
29-JUN-1999;
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                                        CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
  HQTKCSW 187
                                                                                                     YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
                         cspghfcivqdgdhcaacrayatsspgqrvqkggtesqdtlcqncppgtfspngtleecq
                                                                             yrvkeacgeltgtvcepcppgtyiahlnglskclqcqmcdpamglrasrncsrtenavcg
                                                                                                                                meppgdwgpppwrstprtdvlrlvlyltflgapcyapalpsckedeypvgseccpkcspg
                                                                                                                                                                                    184;
                                                                                          Conservative
                                                                                                                                                                                                67.2%;
98.4%;
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                                                                                                                                                                                    Mismatches
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Sequence

197 AA;

Search completed: January 24, 2002, 16:21:43 Job time: 33 sec

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Minimum DB
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Perfect score:
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RESULT 2
US-09-33-279-2
; Sequence 2, Application US/09333279
; Patent No. 6303336
; GENERAL INFORMATION:
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US-08-509-024-2
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7,	Sequence 7, Appli	Sequence 49, Appl	Sequence 4, Appli	Sequence 1, Appli	Patent No. 5395760	Sequence 2, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 48, Appl				

ALIGNMENTS

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Sequence 2, Application US/08509024B
Patent No. 6291207
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/08/509,024B
CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-08-509-024-2
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181 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
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Best Local Similarity
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas E.
REGISTRATION UMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
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Y: U.S.A.
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                                                                    (312) 616-5460
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RESULT 4
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; Sequence 7, Application US/08509024B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SPEAR, PALTICIA G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS
FILE REFERENCE: 0290-1
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 419
TYPE: PRT
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                            HQTKC 185
                                                                                                                  YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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GENERAL INFORMATION:
APPLICANT: BUSÍGLI, Samantha J.
APPLICANT: BUSÍGLI, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HI
TITLE OF INVENTION: PROTEIN FAMILY AND USES 1
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEO ID NOS: 25
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 2
LENGTH: 193
                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-146-950-2
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                                                                                                                          Query Match
Best Local S
Matches 184
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CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 419
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Best Local
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERDES VIRUS ENTRY RECEPTOR PROTEIN
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ORGANISM: Homo sapiens
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                                                             MEPPGDMGPPPMRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
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98.4%;
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                                                                                                                                       Score 1068; DB 'Pred. No. 1e-88;
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US-09-146-950-18
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 197
TYPE: PRT
                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
Query Match
Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                             APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 09404/057001

CURRENT APPLICATION NUMBER: US/09/146,950A

CURRENT FILING DATE: 1998-09-03
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Best Local Similarity
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                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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98.4%;
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                   53.7%;
98.0%;
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 Score 847; DB 4;
Pred. No. 5.7e-69;
1; Mismatches 2
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Pred. No. 5.
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APPLICANT: BUSfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
                                                                                                            NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 77
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 20
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09146950A Patent No. 6287808
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                   APPLICANT: Busfield, Samantha J.
                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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98.0%;
23.1%;
95.5%;
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Pred. No. 3.1e-68;
1; Mismatches C
Score 365; DB 4;
Pred. No. 4.9e-26;
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Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy
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FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FRAGMENT TYPE:
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CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
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REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: 1
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CITY: Boston
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CSTVGLIIC-----VKR--RKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTT 266
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                                                                                                                  VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVICGLKSRMRALLVI 198
                                                                                                                                                                               LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815,
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
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APPLICANT: Rabizadeh,
TITLE OF INVENTION: PO
TITLE OF INVENTION: PO
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226
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.1 Local Similarity 26.1
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                                                                                                                                                                                                                                                                                                                     20 VLRLVLYLTFLGAPCYAPAL-----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                             CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
                                                                                                                                                                                                                                                                                     MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                   ATVIEALQAPPDV---
                                                                      Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA---
                                                                                                     AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE 251
                                                                                                                                         CESCYLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ 175
                                                                                                                                                                                                               CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
                                                                                                                                                                                                                                               CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVVMGILITIFGVFLYIKKVVKKPKDN--EMLPPAARRQDPQEME---
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United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09041886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bredesen, Dale E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           535-8949
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                                                                                                                                                                                                                                                                                                                                                                         17.0%;
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                                                                                                                                                                                                                                                                                                                                                        50;
                                 -TTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                      Score 267.5; DB 4;
Pred. No. 1.3e-16;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dependence
ds of Use
                                                                      ILLVLVFIKKVAKKPTNK 225
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Best Local Similarity
Thehes 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09042785A Patent No. 6194151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Busfie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION UMBER: US OF APPLICATION NUMBER: US OF APPLICATION NUMBER: US OF APPLICATION NUMBER: 26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
   226
                                     252
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                                                                                                                                              116
                                                                       176 Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA--
                                                                                                                                                                              135 CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
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CITY: I
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FILING DATE: 17-MAR-1998
                                                                                                                                                                                                                                                       75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                       CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                     ATVIEALQAPPDV-----
                                                                                                         AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE
                                                                                                                                            CESCYLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ
                                                                                                                                                                                                                   CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
                                                                                                                                                                                                                                                                                         MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
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internal
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                                     -TTVAVEETI 273
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                           ILLVLVFIKKVAKKPTNK
                                                                                                                                                                                                                                                                                                                                                                                                  Length 277;
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RESULT 14 US-09-006-353A-10 ; Sequence 10, Application US/09006353A

Patent No. 6261801

GENERAL INFORMATION:

APPLICANT:

WEI, YING-FEI YU, GUO-LIANG GENTZ, REINER

APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
NUMBER OF SEQUENCES: 26

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RESULT 15
US-08-974-022-47
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                                                   Sequence 47, Application US/08974022 Patent No. 6015938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
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LENGTH: 277 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                             176 Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA----
                                                                                                                                                                                                                                                                 192 AGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGE 251
                                                                                                                                                                                                                                                                                                                                     135 CAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSW--LVTK 191
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STREET: 9410 KEY
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROUKES, AREGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: PF341
                                                                                                                                                                                                                                                                                                                                                                                                         75 CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VLRLVLYLTFLGAPCYAPAL-----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                             AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                                                                                                                                                                                                                                                                                  CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ
                                                                                                                                                                                              ATVIEALQAPPDV-----TTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                                        CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
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9410 KEY WEST AVENUE
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Boyle,
Lacey,
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                Willaim J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 267.5; DB 4; 26.1%; Pred. No. 1.3e-16; tive 50; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10:
                                                                                                                                                                                                                                 -ILLVLVFIKKVAKKPTNK 225
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Search completed: Job time: 52 sec

January 24,

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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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177 LYPVNETSCT---TTAG 190
                                  180 --- QHQTKCSWLVTKAG 193
                                                                      118 NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPPHTYSDSLSPTERCGTSFNYISVGFN 176
                                                                                      60
                                                                                                                                                            74 VCEPCPPGTYIAHLNGLSKCLQCQMCDPAMG-LRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                         20 VLRLVLYLTFLGAPCYAPALP-----SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT 73
                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                       1 MLRLIALLYCY-VYYYGDDYPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLCGPGSNT 59
                                                                                                                                      VCSPCEDGTFTASTNHAPACVSCR--GPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                               207 amino acids
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Chang, Ming-Shi
VENTION: OSTEOPROTEGERIN
                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                         16.5%; Score 260; DB 3; 31.5%; Pred. No. 4.4e-16; tive 25; Mismatches 80;
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                                                                                                                                                                                                                                                                                                          Length 207;
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
    US-08-741-095B-26
1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 24, 2002, 16:21:15; Search time 97.61 Seconds (without alignments) 805.009 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pending_Patents_AA_Main:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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                 /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-342-767-13	US-08-987-902-1	US-08-741-095B-26	US-08-464-595-2	US-08-462-962-2	US-08-462-315-2	PCT-US99-20180-13	PCT-US95-05058-2	PCT-US01-26396-31	ID		
Sequence 13, Appl	Sequence 1, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 2, Appli	Sequence 31, Appl	Description		

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0;

Mismatches

0;

Gaps

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-09-480-284-1 -09-83-262-26 -09-886-342-66 -09-886-342-60 -09-886-342-60 -09-886-342-60 -09-886-342-60 -09-935-727-31 -08-741-095A-2 -08-741-095A-2 -08-741-095B-2 -09-340-690-2 -09-340-690-2 -09-32-22-2 -09-33-262-2 -09-33-262-2 -09-760-455-73 -09-760-455-73 -09-7760-35-874 -09-072-993-2 -09-072	24	ر د د	17	ب	17	$\vdash$	17	↦	17	μ.	17	<u>_</u>	13	14	14	14	14	21	21	24	24	19	18	17	17	11	11	11	11	Н	23	22	22	19	18
	-60-142-657-5	-60-137-457-5	-09-342-767-3	-US99-20180-3	-09-342-767-1	-US99-20180-1	-09-342-767	-US99-2018C	-09-342-767-4	-US99-20180-4	-09-342-767-4	-US99-20180-4	-08-955-5	-09-072-993B-	-09-072-993	-09-072-993C-	-09-072-993-	-09-760-485-87	-09-760-455-7	-60-135-169	-60-125-683	-09-533-262	-09-403-815	-09-340-690-2	-09-340-690-2	-08-741-095B-2	-08-741-095A-2	-08-741-095A-	08-741-095	US96-18540-2	-09-935-727-	-09-886-342-	S-09-882-636-	8-09-533-262-	IS-09-480-284-
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## ALIGNMENTS

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PCT-US01-26396-31
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; Sequence 31, Application PC/TUS0126396
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta; FILE REFERENCE: PF454PCT3
Query Match
Best Local Similarity
Matches 283; Conserv
                                                                                                                                                                                                                              SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US01/26396
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR PRIOR APPLICATION NUMBER: 60/227,598
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-08-25
                                                                                                                                       LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
100.0%;
llarity 100.0%;
Conservative 0
                     Score 1578; DB 1;
Pred. No. 3.6e-119;
                                             Length 283;
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PCT-US95-05058-2
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                                                                                                                   Query Match
Best Local S
Matches 283
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                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKI
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTMARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 0 CITY: ROSELAND
CITY: NEW JERSEY
CTATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW COUNTRY: US ZIP: 07068
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                              61
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                         TOPOLOGY: LI
                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Concu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CARELLA, BYRNE, BAIN, GILI
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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                                                         MEPPGDMGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
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             YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                     283;
                                                                                                                     Conservative
                                                                                                                                                                                                                            LINEAR
                                                                                                                                                                                                                                                                    AMINO ACIDS
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                                                                                                                   0;
                                                                                                                Score 1578; DB 1;
Pred. No. 3.6e-119;
; Mismatches 0;
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                                                                                                                                             Length
                                                                                                                   Indels
                                                                                                                                                 283;
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US-08-462-315-2

Sequence 2, Application US/08462315 GENERAL INFORMATION:

APPLICANT: NI, ET AL.
TITLE OF INVENTION: TU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE:

CARELLA, BYRNE, BAIN, GILFILLAN,

Tumor Necrosis Factor Receptors

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PCT-US99-20180-13
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GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE H
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 09404/079W01
CURRENT APPLICATION NUMBER: PCT/US99/20180
CURRENT FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 58 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILING DATE: 1999-66-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                  121
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                                                                                                                                                                                                                                                                   CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH
                                                               VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                                                                                                CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                               HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                                                                                                                                   YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                         Score 1578;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                       DB 1;
3.6e-119;
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283
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CITY: ROSELAND STATE: NEW JERSEY

ADDRESSEE: STREET: 6

E: CECCHI, STEWART & OLSTEIN 6 BECKER FARM ROAD

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                                                                                                                                                                                     US-08-462-962-2
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                                                                                               Sequence 2, Application US/08462962
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201-994-1700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/462,315
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION UNITA:
PRIOR APPLICATION UNITA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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                                                 ADDRESSEE:
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REFERENCE/DOCKET NUMBER: 325800-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/05058 FILING DATE: 27 APR 95
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                                                                                                                                                                                                                                                                                                                      CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
                                                                                                                                                                                                                                                                                                                                                                                           CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
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                 ROSELAND
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NEW JERSEY
                              E: CARELLA, BYRNE, BAIN, GILI
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
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                                                               GILFILLAN
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                                                                                                                                                                                                                                                                                            RESULT 6
US-08-464-595-2
                                                                                                                                                                                                                                  Sequence 2, Application US/08464595
GENERAL INFORMATION:
APPLICANT: JIAN NI, REINER GENT
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Best Local Similarity
Matches 283; Conserv
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US95/05058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                          ZIP: 07068
                                                          COUNTRY:
                                                                              STREET: 6 BECK:
CITY: ROSELAND
STATE: NEW JER:
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                                                                                                                                     ADDRESSEE: CECCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PC FILING DATE: 27 APR 95
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SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                       ADDRESSEE:
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                                                                              NEW JERSEY
                                                                                                                   6 BECKER FARM ROAD
                                                            USA
                                                                                                                                                                                                                JIAN NI, REINER GENTZ AND CRAIG ROSEN VENTION: Tumor Necrosis Factor Receptors
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                                                                                                                                     CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
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Gaps

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SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:

WORD PERFECT 5.1

US/08/464,595

MS-DOS

OPERATING SYSTEM:

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SOFTWARE:
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Best Local
                                            PRIOR APPLICATION NUMBER: US 08/464,595
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,962
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,315
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-04-27
                                                                                                                                                                                                    TITLE OF INVENTION: Human Tumor Necrosis FILE REFERENCE: 1488.0770004 CURRENT APPLICATION NUMBER: US/08/741,095B CURRENT FILING DATE: 1996-10-30
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                NUMBER OF SEQ ID NOS:
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FILING DATE: APPLI 27, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 33,073
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TOPOLOGY: LI
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                                                                                                                                                                                                                                                                                  Rosen, Craig
Gentz, Reiner
              PatentIn version 3.0
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; LENGTH: 283 amino
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-987-902-1
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APPLICANT: Avi J.
Query Match
Best Local Similarity
Matches 283; Conserv
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Best Local Similarity
Matches 283; Conserv
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LENGTH: 283
                                                                                                                                                                             TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Avi J. Ashkenazi and Scot A. Marsters TITLE OF INVENTION: HVEM Polypeptides and Uses THE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
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                                                                                                                                                                                                                                                  NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600 REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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100.0%; Score 1578; DB 13; 100.0%; Pred. No. 3.6e-119; tive 0; Mismatches 0;
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LENGTH: 283
TYPE: PRT
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Best Local
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TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: MBIO98-061CP1
CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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241
                              241 VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
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                                                                                                                         CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ 180
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VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                            HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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                                                                                                                                                                                                                                                                                                                      100.0%; Score 1578; DB 17; ilarity 100.0%; Pred. No. 3.6e-119; Conservative 0; Mismatches 0;
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           Sequence 26, Application US/09533262 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi and Scot A.
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Best Local
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
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TELEFAX: 650/952-9881
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RESULT

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APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/987,902
FILING DATE: 10-DEC-1997
ATTORNEY/ACENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REGENENCE COCKET NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/480,284 FILING DATE: 10-Jan-2000 PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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     Tumor Necrosis Factor Receptor-Like
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; SOFTWARE: PatentIn Ver. 2
; SEO ID NO 26
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-262-26
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                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local S
Matches 283
                                                                                                                                                                                                                                                                                                           Sequence 46, Applica GENERAL INFORMATION:
APPLICANT: WOO', WILLIAM, I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P2509RIC1
CURRENT APPLICATION NUMBER: US/09/882,636
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/112,850
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EARLIER APPLICATION NUMBER: PCT/US95/05058
EARLIER FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Goddard, Audre
APPLICANT: Gurney, Austin
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APPLICATION NUMBER: US 60/125,683
FILING DATE: 1999-03-22
APPLICATION NUMBER: US 08/741,095
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APPLICATION NUMBER: US 08/462,315
FILING DATE: 1995-06-05
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APPLICATION NUMBER: US 08/464,595
FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/147,383 FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                      Goddard, Audrey
Gurney, Austin L.
Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                    Application US/09882636
                                                                                                                                                                             Roy, Margaret, Ann
                                                                                                                                                                                                 Lawrence, David, A
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OR APPLICATION NUMBER: PCT/US00/13705
OR FILING DATE: May 17, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05840
OR APPLICATION NUMBER: PCT/US00/05004
OR FILING DATE: March 2, 2000
OR FILING DATE: MATCH 2, 2000
OR FILING DATE: FEBRUARY 24, 2000
OR FILING DATE: FEBRUARY 24, 2000
OR FILING DATE: FEBRUARY 24, 2000
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OR APPLICATION NUMBER: 60/069,873
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,702
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,696
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,696
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/066,772
OR APPLICATION NUMBER: 60/063,705
OR APPLICATION NUMBER: 60/032,705
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APPLICATION
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APPLICATION NUMBER: PCT/US00/04342
FILING DATE: February 18, 2000
APPLICATION NUMBER: 09/480,284
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FILING DATE: September 18, 2000
APPLICATION NUMBER: 09/665,350
APPLICATION NUMBER: 09/665,350
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FILING DATE: May 22, 1998
APPLICATION NUMBER: 60/083,500
FILING DATE: APRIL 29, 1998
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APPLICATION NUMBER: 60/107,783
FILING DATE: November 10, 1998
APPLICATION NUMBER: 60/088,742
FILING DATE: June 10, 1998
                                                                                                                                                                             FILING DATE:
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FILING DATE: May 30, 2000
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FILING DATE: April 23, 1998
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FILING DATE: August 23, 2000
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                                             DATE:
                    E: September 15, 19;
N NUMBER: PCT/US99/
E: September 1, 199;
N NUMBER: 09/380/13
                                                                                                          : October 18, 1999
NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                     : December 2, 1999
NUMBER: 09/423,844
                                                                                                                                                                                                                                                                                                                                                                      : January 10, 2000
NUMBER: PCT/US99/30095
                                                                                                                                                       NUMBER: 09/403,297
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ORGANISM: Homo
-09-882-636-46
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EQ ID NO 46
LENGTH: 283
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OR APPLICATION NUMBER: PCT/US99/1252
OR FILING DATE: June 2, 1999
OR APPLICATION NUMBER: PCT/US99/08847
OR FILING DATE: April 23, 1999
OR APPLICATION NUMBER: 09/298, 404
OR FILING DATE: April 23, 1999
OR APPLICATION NUMBER: 09/294, 291
OR APPLICATION NUMBER: 09/284, 291
OR FILING DATE: April 12, 1999
OR APPLICATION NUMBER: PCT/US99/05028
OR APPLICATION NUMBER: PCT/US99/05028
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Local Similarity 100.0%; ;
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DR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MATCH 3, 1999
DR APPLICATION NUMBER: PCT/US99/00106
DR FILING DATE: January 5, 1999
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
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FILING DATE: December 16
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FILING DATE: December 10, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US98/19330 FILING DATE: September 16, 1998 APPLICATION NUMBER: 09/065,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: August 9, APPLICATION NUMBER: 09 FILING DATE: August 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US98/25108
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APPLICATION |
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                                                                                                                   HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
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Pred. No. 3.6e-119;
; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/131,022
PRIOR FILING DATE: April 26, 1999
PRIOR APPLICATION NUMBER: 60/131,445
PRIOR FILING DATE: April 28, 1999
PRIOR APPLICATION NUMBER: 60/134,287
PRIOR APPLICATION NUMBER: 60/144,758
PRIOR APPLICATION NUMBER: 60/144,758
PRIOR APPLICATION NUMBER: 60/145,698
PRIOR APPLICATION NUMBER: 60/145,698
PRIOR APPLICATION NUMBER: 08/934,494
PRIOR APPLICATION NUMBER: 08/934,494
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 08/934,821
PRIOR APPLICATION NUMBER: 08/934,949
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 08/930,507
PRIOR APPLICATION NUMBER: 08/930,507
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 08/960,507
PRIOR FILING DATE: September 29, 1997
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PRIOR FILING DATE: December 12, 1996
PRIOR APPLICATION NUMBER: 60/059,115
PRIOR APPLICATION NUMBER: 60/059,115
PRIOR FILING DATE: September 17, 1997
PRIOR APPLICATION NUMBER: 60/059,184
PRIOR APPLICATION NUMBER: 60/059,352
PRIOR APPLICATION NUMBER: 60/059,352
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 60/052,588
PRIOR FILING DATE: September 19, 1997
PRIOR APPLICATION NUMBER: 60/052,037
PRIOR FILING DATE: October 10, 1997
PRIOR APPLICATION NUMBER: 60/063,127
PRIOR APPLICATION NUMBER: 60/064,809
PRIOR FILING DATE: NOVEMBER: 60/064,809
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PRIOR FILING DATE: November
PRIOR APPLICATION NUMBER: 66
PRIOR FILING DATE: December
PRIOR APPLICATION NUMBER: 66
PRIOR FILING DATE: March 13
PRIOR APPLICATION NUMBER: 66
                                                          PRIOR APPLICATION NUMBER: 08/960,507
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: PCT/US97/22278
PRIOR FILING DATE: December 5, 1997
PRIOR APPLICATION NUMBER: 08/987,902
PRIOR FILING DATE: December 10, 1997
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: CELL GROWTH
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OR APPLICATION NUMBER: 60/081,071
OR FILING DATE: April 8 1998
OR APPLICATION NUMBER: 60/081,954
OR FILING DATE: April 15, 1998
OR APPLICATION NUMBER: 60/100,858
OR FILING DATE: September 17, 1998
OR APPLICATION NUMBER: 60/113,296
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 60/103,304
OR FILING DATE: November 20, 1998
OR APPLICATION NUMBER: 60/109,304
OR FILING DATE: November 20, 1998
OR APPLICATION NUMBER: 60/130,232
OR APPLICATION NUMBER: 60/130,232
FILING DATE: Decembe APPLICATION NUMBER: FILING DATE: August
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OR APPLICATION NUMBER: 09/333,077
OR FILING DATE: June 14, 1999
OR APPLICATION NUMBER: 09/380,138
OR FILING DATE: August 25, 1999
OR APPLICATION NUMBER: 09/380,139
OR FILING DATE: August 25, 1999
OR APPLICATION NUMBER: 07/05/05/21090
OR REPLICATION NUMBER: 07/05/05/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
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R APPLICATION NUMBER: 09/284,291

R FILING DATE: April 12, 1999

R APPLICATION NUMBER: 09/332,928

R FILING DATE: June 14, 1999

R APPLICATION NUMBER: 09/332,929
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FILING DATE: September 15, 1999
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APPLICATION NUMBER: 09/333,075
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APPLICATION NUMBER: 09/254,465
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FILING DATE: October 9, 1998
APPLICATION NUMBER: PCT/US98/24855
FILING DATE: NOVember 20, 1998
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FILING DATE: October 9, 1998
APPLICATION NUMBER: 07, 1998
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    : January 5, 2000

! NUMBER: PCT/US00/00277

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N NUMBER: 09/480,284
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: 09/808,689
PRIOR FILING DATE: March 14, 2001
NUMBER OF SEQ ID NOS: 79
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PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
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OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/15264
IOR FILING DATE: June 2, 2000
IOR APPLICATION NUMBER: 09/664,610
IOR FILING DATE: September 18, 2000
IOR APPLICATION NUMBER: 09/665 350
IOR FILING DATE: September 18, 2000
IOR APPLICATION NUMBER: 09/690,169
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APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/06884
FILING DATE: March 15, 2000
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RESULT 14 US-09-935-727-31

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Sequence 31, Application US/09935727 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc.

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LENGTH: 283
TYPE: PRT
                                                                                              Sequence 2, Application GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
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CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
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           APPLICANT:
APPLICANT:
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 APPLICANT:
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APPLICATION NUMBER: 60/121,774
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APPLICATION NUMBER: 60/
FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/146,371 FILING DATE: 1999-08-02 APPLICATION NUMBER: 60/131,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/252,131 FILING DATE: 2000-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/
FILING DATE: 1998-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/124,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/227,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/168,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 2000-0:
                                                                                                                                                                                                                                                                                                                                                        HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
                                                                                                                                                                                                                                                                                                                CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSDNGTLEECQ 180
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King of Prussia, PA 1940
United States of America
                       Rockville, MD 20850
United States of America
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1578; ilarity 100.0%; Pred. No. 3. Conservative 0; Mismatches
                                                                9410 Key West Avenue
                                                                                  Human Genome Sciences,
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              PA 19406
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; MOLECULE TYPE: protein PCT-US96-18540-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
NAME: Goldstein, Jorge A.
14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Tumor No TITLE OF INVENTION: Receptor-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gentz, Reiner L.
APPLICANT: Lyn, Sally Doreen Patricia
APPLICANT: Hurle, Mark Robert
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                                                                                      181 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS 240
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ZIP: 20005-3934
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                                    VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
                                                                                                                                                                                                                     YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
                                                                                                                                            CSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQ
                                                                                                                                                                                                                                          YRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCG 120
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MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG
                                                                       HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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1100 New York Ave, Suite
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 6.2e-119;
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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ALIGNMENTS

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SOFTWARE: PatentIn Ver.;
SEQ ID NO 2;
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-924-231-2
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Best Local Similarity
Matches 283; Conserv
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PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Date: 1997-08-15
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
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CURRENT FILING DATE: 2001-08-08
181 HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS
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GENERAL INFORMATION:

APPLICANT: SPEAR, Patricia G.

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LENGTH: 277
TYPE: PRT
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILLING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/054,488
PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NOELLE, RANDOLPH J.
APPLICANT: BURNS, CHRISTOPHER M.
TITLE OF INVENTION: USE OF ANTI-GP-39 ANTIBODIES FOR TREATMENT AND/OR
TITLE OF INVENTION: REVERSAL OF LUPUS AND LUPUS ASSOCIATED KIDNEY DISEASE
FILE REFERENCE: 037003-0280622
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 08/742,480 PRIOR FILING DATE: 1996-11-01 PRIOR APPLICATION NUMBER: 08/338,975 PRIOR FILING DATE: 1994-11-14
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1992-02-14 NUMBER OF SEQ ID NOS: 2
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CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 5.5e-16;
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Best Local S
Matches 59
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                                           APPLICANT: Murphy, Erin E.
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related Reagents
FILE REFERENCE: SF0818K
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/852,455
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/202,912
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 81
                     CURRENT APPLICATION NUMBER: US/09/840;795
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APPLICANT: PRENDERGAST, JOHN
TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
FILE REFERENCE: 2598-4004US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BLUME, ARTHUR J. APPLICANT: GOLDSTEIN, NEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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nes 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 122
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2001-04-23
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APPLICANT: BURSTein, Haim
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOW
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FAC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
            RESULT 7
US-09-896-096A-17
Sequence 17, Application US/09896096A
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-10
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; ORGANISM: primate
US-09-840-795-10
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 225
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Best Local Similarity
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APPLICANT: ASHKENAZI, AVI J
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                                                                                                                                        146 PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 PGFGVARPGTETSDVVCKPCAPGTESNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS 204
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Local Similarity 32.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                 59;
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Pred. No. 2.4e-15;
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QY
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TYPE: PRT
ORGANISM: Homo sapien
US-09-579-845-1
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                                                              Best Local Similarity 32.8 Matches 59; Conservative
                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ
SEQ ID NO 1
                                                                                   Query Match
Best Local
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PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PRIOR SOFTWARE:
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APPLICANT: Stepan, Anthony M.
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
CURRENT FILING DATE: 2000-05-26
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APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
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35 YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKBACGELTGTVCEPCPPGTYIAHLNGLS 91
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nes 59; Conserv
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WOOD, WILLIAM I.
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LAWRENCE, DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DODGE, KELLY H.
GURNEY, AUSTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PITTI, ROBERT
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                                                                                                                                                                                                                                                                      for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 259; DB 5; L
32.8%; Pred. No. 4.9e-15;
32.8%; Mismatches 76;
                                                              16.4%; Score 259; DB 5; I 32.8%; Pred. No. 5.5e-15; tive 23; Mismatches 76;
                                                                                                                                                                                                                                                                      4.0
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                                                                                                     Length 518;
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                                                              Indels
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                                                              Gaps
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-3
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Best Local Similarity 32.8
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
                                                                                                                                                                                             APPLICANT:
                                                                        TITLE OF INVENTION: DCR3 POlypeptide, A TNFR Homolog FILE REFERENCE: P1134R2 REVISED CURRENT APPLICATION NUMBER: US/09/896,096A CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                    APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
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APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS
TITLE OF INVENTION: DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 226272004420
CURRENT APPLICATION NUMBER: US/09/579,845
CURRENT FILING DATE: 2000-05-26
PRIOR FILING DATE:
                  PRIOR APPLICATION NUMBER: US 60/059,288
                                    PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 KCLQCQMCDPAMGLRASRN------CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECLSC------GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCLQCQMCDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                                                                     Application US/09896096A
                                                                                                                                                       TUMAS, DANIEL B WOOD, WILLIAM I.
                                                                                                                                                                                             PITTI, ROBERT ROY, MARGARET A
                                                                                                                                                                                                                                    LAWRENCE,
                                                                                                                                                                                                                                  DAVID A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.4%; Score 259; DB 5; Length 518; 32.8%; Pred. No. 5.5e-15; ative 23; Mismatches 76; Indels
                                                        us 09/157,289
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; NAME/KEY: misc_feature ; LCCATION: (79) ; OTHER INFORMATION: Xaa at residue 79 US-09-840-795-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application us/
GENERAL INFORMATION:
APPLICANT: Murphy, Erin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 300
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: primate FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
126 FCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 TALGLALNVPGSSSH 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 SWLVTKAGAGTSSSH 200
                                                                                                                                                                                                                                                          Local Similarity
nes 69; Conserv
                                                                      64 RDSPMTCGPCPPRHYTQFWNYLERCRXCYVLC----GEREEEARACHATHNRACRCRTGF 119
                                                                                                                                                                                                             16 PRIDVLRLVLYLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSPGYRVKEACG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RDSPTTCGPCPPRHYTQFWNYLER----CRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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                                                                                                                   ELTGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLR--ASRNCSRTENAVCGCSPGH 125
                                                                                                                                                                PGLSLLCLVLALPAL---LPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSSEQCQPHRNC 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09840795
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Bates, Elizabeth Esther Mary
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                                                                                                                                                                                                                                                          Conservative
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35.2%;
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                                                                                                                                                                                                                                                        ; Score 239; DB 5;
; Pred. No. 1.7e-13;
15; Mismatches 88
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RESULT 13
US-09-579-845-14
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US-10-003-211-1
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                                                                                                JENERAL INFORMATION.

APPLICANT: Burstein, Haim
APPLICANT: Stepan, Anthony M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (7

TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 22627200420

CURRENT APPLICATION NUMBER: US/09/579,845

"""" FILING DATE: 2000-05-26
              SEQ ID NO 14
LENGTH: 487
                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09579845 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                        CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/150,688
PRIOR FILING DATE: 1999-05-28
                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US97/19436
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/029,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: A013US
CURRENT APPLICATION NUMBER: US/10/003,211
CURRENT FILING DATE: 2001-10-31
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TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and
TITLE OF INVENTION: Anti-Lymphotoxin Receptor and Ligand
TITLE OF INVENTION: Therapeutic Agents for the Treatment
TITLE OF INVENTION: Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Biogen, Inc. APPLICANT: Browning, 6
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TYPE: PRT
TYPE: PRT
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56; Conserv
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                                                     20
Windows Version 4.0
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Pred. No. 6.2e-13;
Mismatches 66;
                                                                                                                                                                                                             FACTOR (TNF) IN TNF-ASSOCIATED
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; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-579-845-7
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Best Local Similarity 25.4
Conservative
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/579,845

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/150,688

PRIOR FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Burstein, Haim
APPLICANT: Stepan, Anthony M.
APPLICANT: Stepan, Anthony M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF)
TITLE OF INVENTION: DISCRERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
  216 IYVSQPEP--
                                                                                                                                                               112 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF
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                                                                                                                                                                                                                                                  54 CCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQ--VETHNC
                                                                                                                                                                                                                                                                                      53 CCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQC-QMCDPAMGLRASRNC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 CCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQC-QMCDPAMGLRASRNC
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                                                                                                              S-PNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVC-----STVGLI
                                      ICVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTG 278
                                                                                                                                                                                                         SRTENAVCGCSPGHFCIVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTF 170
                                                                                  SDTTSSTDVCRPHGICSILAIPGNASTDA---
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                                                                                                                                                                                                                                                                                                                               13.8%; score 217; DB 5; 25.4%; Pred. No. 1.2e-11; tive 29; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TRSQPMDQEPGPSQTPHIPVSLGSTPIIE--PSITGGVPR
-TRSQPMDQEPGPSQTPHIPVSLGSTPIIE--PSITG
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                                                                                  ----VCASESPTPSAVPRT
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FILE REFERENCE: SF0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 227
TYPE: PAT
ORGANISM: rodent
US-09-840-795-9
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Search completed: January 24, 2002, 16:22:45 Job time: 90 sec
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US-09-840-795-9
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GENERAL INFORMATION:
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE DEFERENCE: GENOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match : 13.5%; Score 213.5; DB 5; Length 227; Best Local Similarity 28.5%; Pred. No. 2.1e-11; Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps
                                                                                                     188 SILAIPGNASTDA 200
                                                                                                                                                                                  128 ALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRIC 187
                                                                                                                                            186 SWLVTKAGAGTSS 198
                                                                                                                                                                                                        11 VFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNK 70
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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 16.4
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## ALIGNMENTS

A46476

A; Molecule type: nucleic acid
A; Residues: 1-287, Irv' <GRI>A; Cross-references: GB: M83312; NID:g1553058; PIDN:AAB08705.1;
A; Cross-references: GB: M83312; NID:g1553058; PIDN:AAB08705.1;
A; Experimental source: BALB/c; liver
A; Note: sequence extracted from NCBI backbone (NCBIP:120357)
C; Comment: For an alternative splice form, see PIR:A46515.
C; Comment: For an alternative splice form, see PIR:A46476.
C; Superfamily: CD27 antigen; Respector repeat homology
C; Keywords: alternative splicing; transmembrane protein
F; 105-144/Domain: NGF receptor repeat homology <NGF> A;Cross references: GB.M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Co
J.Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586
A;Accession: A46515 J. Immunol. 148, 620-626, 1992 A;Title: Differential increase of an alternatively polyadenylated mRNA species of mur A;Reference number: A46476; MUID:92105763 A;Accession: A46476 B cell-associated surface molecule CD40, long spilce form - mouse C; Species: Mus musculus (house mouse) C;Date: 18-Jun-1993 "sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000 C;Accession: A46476; A46515 Qy B Ş 뫄 ρy В Š A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA A; Residues: 1-305 < TOR> A;Status: preliminary R; Torres, R.M.; Clark, Query Match Best Local S Matches 69 216 CSTVGLIIC-----VKR--RKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTT 266 101 161 LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215 25 41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100 PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160 TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84 VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVICGLKSRMRALLVI PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD----CEACAQHTPCIPGFGVMEMATETTDT 69; Similarity 27.9 69; Conservative E.A 17.5%; 27.9%; 43; Score 276.5; DB 2; Length pred. No. 2.9e-13; Mismatches 106; Indels 305; PID:g1553059; GB:M94126 29; Gaps 141 198 Cockay .

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RESULT 3
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane
F;1-20/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 8, 1403-1410, 1989
A; Title: A B-lymphocyte activation molecule
A; Reference number: S04460; MUID:89356608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change
C;Accession: S04460; A60771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;21-277/Product: B-cell activation protein CD40 *status experimental <MAT>F;21-193/Domain: extracellular *status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Biochemical characteristics and partial amino acid sequence A; Reference number: A60771; MUID:89093941
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A; Residues: 1-277 <STA>
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                                                                                                                                                                                                             Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA----
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                                                                                                                            AP--HPKQEPQEINFPDDLPGSNTAAPVQETL
                                                                                                                                                                                                                                                                                                                                                                                        CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
                  rabbit fibroma virus
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                                                                                                                                                                    -TTVAVEETI 273
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35556; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R
Science 248, 1019-1023, 1990
                                                A; Molecule type: mRNA;
A; Residues: 23-461 < DE
                                                                                                                                                            A; Title: Two human TNF receptors have similar extracellular, A; Reference number: A48416; MUID:91370690
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-195, 'R', 197-461 < KOH>
A; Cross-references: GB: M55994; GB: M38549; NID: g339757; PIDN: AAA36755.1; PID: g339758
A; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhau
Cytokine 2, 231-237, 1990
                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186 R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990 A;Title: A second tumor necrosis factor receptor gene product can shed a A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-461 <SMI>
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A;Accession: A35356
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C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                      A; Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-325 <UPT>
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 VCEPCPPGTYIAHLNGLSKCLQCQMCDPAMG-LRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VLRLVLYLTFLGAPCYAPALP-----SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- OHOTKCSWLVTKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEEC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLRLIALLYCY-YYYYGDDYPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLCGPGSNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                23-461 <DEM>
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31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
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Pred. No. 4.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.K.; Squir
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R;Kuhnert, P.; Kemper, U.; warrow. .
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization
A;Title: Cloning, sequencing and partial functional characterization
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J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215
A;Accession: B35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Nolecule type: protein
A; Nolecule type: protein
A; Residues: 23-40;65-69;136-141;300-306
A; Residues: " Nowick D.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; MoLecule type: mRNA
A; Residues: 116-140, 'p', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A; Residues: 16-140, 'p', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A; Cross-references: GB: M35857; NID: g339751; PIDN: AAA63262.1; PID: g339752
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.
J. Biol. Chem. 265, 20131-20138, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and A;Reference number: A36007; MUID:90349572
A;Accession: A36007
                                                                                                                             뮹
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F;164-201/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F; 23-416/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid
A;Reference number: A23666; MUID:91056048
A;Accession: A23666
hypothetical
                            T28623
                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the list of introns is incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 26/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1p36.2-1p36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 27-31 <ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology; superfamily: tumor necrosis factor, receptor; transmembrane protein; keywords: duplication; glycoprotein; receptor; transmembrane protein; 1-22/Domain: signal sequence #status: predicted <SIG>; 23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171,193/Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262-279/Domain:
                                                                                                                             145
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                                                 и
                                                                                                                                                                            PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199
                                                                                                                                                                                                                             ECLSC-----GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144
                                                                                                                                                                                                                                                                            KCLQCQMCDPAMGLRASRN-----CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145
                                                                                                                                                                                                                                                                                                                              YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
                                                                                                                                                                                                                                                                                                                                                           YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91
                                                                                                                             PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane #status predicted <TMN> intracellular #status predicted <INT>
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  G2R -
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variola major virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 259; DB 1;
Pred. No. 7.7e-12;
3; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 461;
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C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir A;Reference number: Z20488; MUID:94088747
A;Accession: T28623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to GenBank, March 199
A;Description: Analysis of the
A;Reference number: A72150
A;Accession: D72175
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: G2R C;Superfamily: myxoma virus T2 protein; NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics: A; Gene: G2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; A;Experimental source: strain Garcia-1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-349 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                           21 LRLVLYLTFLGAPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLLK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
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                                                                                                                                                                                                                                                                                                                                         Local
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                                                  QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-----PNGTLE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDVEITLYPVNDTSCTRTTT---TGLSES----ILTSELTITM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFNY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQ 130
KGSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSYTVSSTDKCEPVPNNTFN
                                                                                                                                                                                                           MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKSVLYLYILFLSCIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKT
                                                                                                     TNTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYYCLL 118
                                                                                                                                                        TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                           66; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov,
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -HOTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVI 214
                                                                                                                                                                                                                                                                                                                                      16.3%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete coding sequence of DNA of alastrim variola
                                                                                                                                                                                                                                         ---YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                                                                                                                                                                                              23;
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                                                                                                                                                                                                                                                                                                           Score 257; DB 2;
Pred. No. 8.5e-12,
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 7.8
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 257.5;
Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8e-12;
nes 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat homology
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                         Gaps
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177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytcrov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: B28R protein (COP)
C;Speciles: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                              日
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 31-168 <SHC>
A; Cross-references: EMBL: X69198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S32385; MUID:93202281
A;Accession: S32385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to GenBank, November 1992 A; Reference number: A36859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; A;Experimental source: strain India-1967, isolate Ind3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-349 < KOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S46888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-349 <BLI>
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A; Status: preliminary
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Best Local S
Matches 66
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                     necrosis
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                                                                                                                                        178 YIDVEITLYPVNDTSCTRTTT-
                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LRLVLYLTFLGAPC-----
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                                                                                                                                                                                                                             KGSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFN
                                                                                                                                                                                                                                                                                                                  THTQCTPCGSGTFTSRNNHLPACLSCNGRCN--SNQVETRSCHTTHNRICECSPGYYCLL 118
                                                                                                                                                                                                                                                                                                                                                               TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                                                                                                                         MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK 60
                                                                                                                                                                                                                                                                     QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS------PNGTLE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                     factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source: strain India-1967, ssp. major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variola virus
                                                                                                                                                                              --HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVI 214
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                     receptor
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                     2-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                      ---TGLSES-----ILTSELTITM 214
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Pred.
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No. 8.
                     protein
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.5e-12;
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Query Match

Best Local Similarity Matches 51; Conserv

Conservative

16;

Pred. No. 1.16 5; Mismatches Score 240.5;

1.1e-10;

Indels

25;

Gaps

5

DВ 2;

Length 271;

15.2%;

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A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897 C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: growth factor receptor; transmembrane protein F;1-19/Domain: signal sequence #status predicted <SIG>F;20-271/Product: OX40 antigen #status predicted <MAT>F;211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: nerve growth factor receptor homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text C;Accession: S12783; S08036 R;Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                                                                                                                                                                A; Title: Characterization of the MRC OX40 A; Reference number: $12783; MUID:90214614 A; Accession: $12783
                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-271 <MAL>
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A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq A;Reference number: I54182; MUID:93252381
A;Accession: I54182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OX40 antigen precursor - rat
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C;Genetics:
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A; Residues: 1-435 < RE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVLLPLAFFLLLATVFSCIWKSHP--SLCRKLGSLLKRRPQGEGPNPVAGSWEPPKAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAGHFQNTSSPSA---RCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGTF----SPNGTLEECQHQTKC-SWLVTKAGAGTSSSHWVWW------FLSGSLVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSKRKTQCRCQPGMFCAAW-ALECTHCELLSDCPPGTEAELKDEVGKGNNH-----CVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPG-----QRVQKGGTESQDTLCQNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-435 <RES>
3-435 = 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-435 | 1-
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26.7%;
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Pred. No. 2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                             PID:957831
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RESULT 10
GOVZML
T2 protein -
                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; 534377
C;Accession: J. E.; Van den Eertwegh, A.J.; Claassen, E.; Noelle, R;Calderhead, D.M.; Buhlmann, J.E.; Van den Eertwegh, A.J.; Claassen, E.; Noelle, J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse 0x40: a T cell activation marker that may mediate T-B ce
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C;Keywords: glycoprotein
F;66-105/Domain: NGF receptor repeat homology <NG3>F;106-147/Domain: NGF receptor repeat homology <NG3>F;66,181,205,238/Binding site: carbohydrate (Asn) (co
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                           A;Reference number: I48700; MUID:94044750
A;Accession: I48700
                                                                                                                                                                                                                                                                                              gene ox40 protein - mouse N;Alternate names: OX40 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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A; Residues: 1-326 < UPT>
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A40566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ------
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translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCSPCKNETFTASTNHAPACVSCRGRC--TGHLSESQSCDKTRDRVCDCSAGNYCLLKGQ 117
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73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TTAGPNEVVKTSEFSVTLNHTDCDPVFHTEYYGTSGSEGAGGFFTGM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 238.5; Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                R.J.;
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A; Residues: 1-22 < KIS>
                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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A; Residues: 1-474 <GOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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Best Local
                           79-120/Domain: NGF receptor repeat
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Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the A;Reference number: I48334, MUID:95255413
A;Status. ***
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991.
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A;Reference number: A38634; MUID:91187885
A;Accession: B38634
                     F;1-22/Domain: signal sequence #status predicted <SIG>F;23-474/Product: tumor necrosis factor receptor type F;40-77/Domain: NGF receptor repeat homology <NGI>
                                                                                                             A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                     A; Description: Characterization A; Reference number: S54816 A; Accession: S54816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Goodwin, R.G.; Anderson, D.; Jerzy, R.;
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression
A;Reference number: A40254; MUID:91246168
A;Accession: A40254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB.M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the BMBL Data Library, May 1995 A;Description: Characterization of the promoter region of the murine p75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor receptor type 2 precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-272 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 HRSGSELKQNCTPTQDTVCRCRPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CVPCPPGHFSP-GNNQACKPWTNCT 146
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D27 antigen; NGF receptor re
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receptor repeat homology
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Pred. No. 7.5e-09;
homology <NG2>
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homology <NG4>

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
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A;Title: Allelic variation of the type 2 tumor necrosis A;Reference number: 148854; MUID:95178848
A;Accession: 148854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I48854
                                                         A; Reference number: JC2395;
A; Accession: JC2395
                                                                                             Biochem. Biophys. Res. Commun. 198, 666-674, A; Title: A variant mRNA species encoding a t
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C; Species: Mus musculus (house mouse)
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A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1;
                      A; Residues: 1-324 <KIM>
                                      A; Molecule type: mRNA
                                                                                                                                                                                                                 Fas antigen precursor - rat
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQC-QMCDPAMGLRASRNC 111
                                                                                                                                                                                                                                                                                                                                                                                              TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILAIPGNASTDA 200
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                                                                                                                                                                                                                                                                                                                   SDTTSSTDVCRPHRICSILAIPGNASTDA 185
                                                                                                                                                                                                                                                                                                                                                      S-PNGTLEECQHQTKCSWLVTKAGAGTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                     SRTENAVCGCSPGHFCIVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSC--STDQVETRAC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWLVTKAGAGTSS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVQ-DGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRA---CTKQQNRVCACEAGRYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTGTVCEPCPPGTYIAHLNGLSKCLQC--QMCDPAMGLRASRNCSRTENAVCGCSPGHFC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                               MUID:94128114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 212.5; DB 2; Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 213.5;
Pred. No. 1.
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  PID:d1005650; PID:g468487
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J. Biol. Chem. 267, 10709-10715, 1992
A;Title: purification and molecular cloning of A;Reference number: A38142; MUID:92268122
A;Accession: A38142
A;Status: preliminary; not compared with conce A;Molecule type: nucleic acid A;Residues: 1-134,'Q','J36-335 <OEH>A;Experimental source: SKW6-4 cells
A;Note: sequence extracted from NCBI backbone A;Note: in NCBI backbone the source is designa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 62/1
C; Superfamily: N
C; Keywords: trar
                                                                                                                                                                                                                                                                                                                                                                                       R; Krammer, P.H. submitted to the EMBL Data Library, submitted to the EMBL Data Library, specific number: $24543
                                                                                                                                                                                                                          A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742 R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, J. Biol. Chem. 267, 10709-10715, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can A;Reference number: A40036; MUID:91309137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: thymus
A; Accession: PC2246
A; Molecule type: mRNA
A; Residues: 1-62, 'RFT' <KI2>
A; Cross-references: DDBJ:D26113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40036; S24543; A38142
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
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F;44-79/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: liver C; Genetics:
                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-335 < KRA>
                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-335 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A40036
                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: surface antigen APO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis-mediating surface antigen Fas precursor .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A40036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 VGLIICVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVCST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCSEGLYQVGPFCCQPCQPGERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT-VCEPCPPG-TYIAHLNGLSKCLQCQM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTKCKK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
  extracted from NCBI backbone (NCBIP:103810) backbone the source is designated as mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 206.5; DB 2
Pred. No. 3.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                              conceptual translation
                                                                                                                                                                                                        of the APO-1 cell surface antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QSSNYKLLWLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
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                                                                                                                                                                                                                                                    G.; Klas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:g182410
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                                                                                                                                                                                                                                                      C.; Li-Weber, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273
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C:Genetics:
A:Gene: GDB:APT1
A:Gross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: NGF receptor repeat homology
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: Signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
Search completed: January 24, 2002, 16:22:25 Job time: 75 sec
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                                                                                                         161 LCQNCPPGTFSPNGTLEEC--QHQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVIVICST 218
:|::| | | | :|::|
                                                                                                                                                                                                        139 VCEHCDPCTKCEHGIIKECTLTSNTKC----KEEGSRSNLGW---
                                                                                                                                                                                                                                                                                                   109 EGHGLEVEINCTRTQNTKCRCKPNFFC------138
                                                                                                                                                                                                                                                                                                                                              101 PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
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Result
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Maximum Match 100%
Listing first 45 summaries
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CD40_BOVIN
VT2_SFVKA
                     TNR1_PIG
TNR1_BOVIN
CD27_MOUSE
TNR1_MOUSE
41BB_HUMAN
CD30_HUMAN
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NGFR_RAT
FASA_BOVIN
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41BB_MOUSE
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9 rattus norv
8 h wsl-1 pro
5 homo sapien
6 mus musculu
rattus norv
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3 shope fibro
3 homo sapien
5 variola vir
1 homo sapien
4 mus musculu
5 rattus norv
yallus yall
homo sapien
rattus norv
homo sapien
mus musculu
sus scrofa
bos taurus
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mus musculu
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## ALIGNMENTS

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s SWISS-PROT entry is copyright. It is produced through a colument the Swiss Institute of Bioinformatics and the EMBL ou European Bioinformatics Institute. There are no restrictlo by non-profit institutions as long as its content is iffied and this statement is not removed. Usage by and for ittes requires a license agreement (See http://www.isb-sib.ch send an email to license@isb-sib.ch).  L; U70321; AAB58354.1;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Zhang W., Wan T., Cao X.;  Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases.  Submitted (NAY-1999) to the EMBL/GenBank/DDBJ databases.  FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.  PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED  THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO  CHO CELLS, AND MEDIATED HSV ENTRY INVO ACTIVATED HUMAN T CELLS.  -!- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).  -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  IN LUNG, SPLEEN, AND THYMUS.  -!- SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.	SEQUENCE FROM N.A.  MEDLINE-97306336; PubMed-9162061;  KWON B.S., Tan K.B., Ni J., Oh KO., Lee Z.H., Kim K.K., Kim YJ.,  Wang S., Gentz R., Yu GL., Harrop J., Lyn S.D., Silverman C.,  Porter T.G., Truneh A., Young P.R.;  "A newly identified member of the tumor necrosis factor receptor superfamily with a wide tissue distribution and involvement in lymphocyte activation.";  J., Biol. Chem. 272:14272-14276(1997).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE-97053782; PubMed-8898196; MEDLINE-97053782; PubMed-8898196; Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.; Montgomery R.I., Warner for the July into cells mediated by a novel member of the TNF/NGF receptor family."; Cell 87:427-436(1996).	20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last sequence update) TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2) (TR2). TNFRSF14 OR HVEM. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	LT 1 _HUMAN _TR14_HUMAN STANDAR Q9295; Q9UM65; 20-AUG-2001 (R61 40)

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Best Local Similarity
                                                                                                                                                                                                           _MOUSE
          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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                                                                                                                 CD40_MOUSE STANDARD; PRT; 289 AA P27512; P27512; O1-AUG-1992 (Rel. 23, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID CARBOHYD
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SMART; SM00208; TNFR; 3.
PROSITE; PS006655.
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203
224
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173
                                                              (Mouse)
                                                                                               el. 38, Last annotation update)
- PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
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                               Chordata;
Rodentia;
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99.6%;
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BY SIMILARITY.
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Pred. No. 5e-120;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 X TNFR-CYS
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS.
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                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                          ĀĀ
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                               Murinae; Mus
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Best Local
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EMBL; M94126; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
PIR; A46476; A46476.
HSSP; P25942; 1CDF
                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001368; TNFR_c6.
pfam; pF00020; TNFR_c6; 4.
proDom; pD000771; TNFR_c6; 1.
smart; SM00208; TNFR; 4.
pROSITE; pS00652; TNFR_NGFR_1; 1.
pROSITE; pS50050; TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93094586; PubMed=1281194; Grimaldi J.C., Torres R., Kozak C.A., Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92105763; PubMed-1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated species of murine CD40 upon B lymphocyte activation.";
Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                         Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                     TRANSMEM
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MGD; MGI:88336; Tnfrsf5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic structure and
                                              101
161
                        85
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LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV
                                              PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                      TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE
                                                                                              SCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
                       PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.M.;
                                                                                                                         69;
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                  B-cell; Glycoprotein;
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27.9%;
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                                                                                                                                                                                     WW;
                                                                                                                       43;
                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
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Pred.
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; C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                               CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                   Transmembrane; Repeat; Signal.
                                                                                                                                   276.5;
No. 1.9
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                                                                                                                         106;
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                                                                                                                       Indels
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MBL outstation -
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CD40_HUMAN
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PROSITE; PROSITE;
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                             InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40".
Protein Sci. 7:1124-1135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
MEDLINE=98266353; PubMed=9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A B-lymphocyte activation molecule relat
factor receptor and induced by cytokines
EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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01-MAY-1992 (Rel.
30-MAY-2000 (Rel.
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                                                                                              PDB; 1CDF; 01-APR-97
MIM; 109535; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction and analysis of a detailed three-dimensional model the ligand binding domain of the human B cell receptor CD40."; proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
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                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH I DATABASE: NAME-PROW; NOTE-CD guide CD40 entry;
                                                                                                                                                                                                                                                                                                    WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
                                                                                                                             S04460;
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                                                                                                                             X60592; CAA43045.1;
S04460; S04460.
PS00652;
PS50050;
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TNFR_NGFR_1;
TNFR_NGFR_2;
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PubMed=9037712;
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Last annotation update)
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CD40_BOVIN
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Q1-NOV-1997 (Rel. 3

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15-JUL-1999 (Rel. 3
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SEQUENCE
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DOMAIN
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REPEAT
REPEAT
                       Hirano A., Brown W.C., Estes D.M.; "Cloning, expression and biological function of the bovine homologue: role in B-lymphocyte growth and differentiation
                                                                                          Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
                  cattle.";
                                                                                                                               CD40L RECEPTOR PRECURSOR TNFRSF5 OR CD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; B-cell; 3D-structure.
Immunology 90:294-300(1997)
                                                      MEDLINE=97281252;
                                                               SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9913;
                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                      252
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                                                                                                                                                                                                                                                                                                                                                                                                        20 VLRLVLYLTFLGAPCYAPAL-----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                    AP--HPKQEPQEINFPDDLPGSNTAAPVQETL 255
                                                                                                                                                                                                                                                                        Q-AGTNKTDVVCGPQDRLRALVVIPIIFGILFA----
                                                                                                                                                                                                                                                                                                                     CEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDH 134
                                                                                                                                                                                                                                                                                                                                                                                       MVRLPLQCVLWG--CLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETE 58
                                                                                                                                                                                                                                                      ATVIEALQAPPDV-----TTVAVEETI
                                                                                                                                                                                                                                                                                                             CESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQ
                                                                                                                                                                                                                                                                                                                                                  CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC----TSEA
                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
71; Conser
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194
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                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                  38,
                                                       PubMed=9135560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%;
26.1%;
                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                   Created)
                                                                                                                                       (B-CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
A CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 267.5; I
Pred. No. 9.6e:
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CD40L RECEPTOR.
EXTRACELLULAR ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . N-LINKED (GLCNAC. . . BC8776EC2C4A5680 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                   Craniata; Vertebrata; Eute
actyla; Ruminantia; Pecora;
                                                                                                                                                                                       PRT;
                                                                                                                                                                                       269
LIGAND KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e-1
                                                                                                                                        ANTIGEN
                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            116;
                                                                                                                                                                                                                                                                        - ILLVLVFIKKVAKKPTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                        CD40) (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
AS CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                             277;
                                                                                                     Bovoidea
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                                                                                                                                                                                                                                                                                          251
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VT2_SFVAN
ID VT2_S
AC P2594
AC P2594
DT 01-MA
DT 01-MA
DT 15-JU
DE TUMOR
GN T2.
OS Shope
CC V1rus
OC Lepor
OX NCBI.
RN [1]
RP SEQUE
RX MEDL1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                 VT2_SFVKA
P25943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
NON_TER
SEQUENCE
SEQUENCE FROM N.A.
MEDLINE-87321103; PubMed=2820128
                                                               Leporipoxvirus.
NCBI_TaxID=10272;
                                                                                                          Viruses; dsDNA viruses,
                                                                                                                              Shope fibroma virus
                                                                                                                                                                              TUMOR NECROSIS FACTOR
                                                                                                                                                                                             01-MAY-1992 (Rel. 22,
01-MAY-1992 (Rel. 22,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bloinformatics and long as its concert as use by non-profit institutions as long as its concert and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO01368; TNFR_c6. pfam; pF00020; TNFR_c6; 4. probom; pD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U57745; AAC48710.1; -. HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                178
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                                                                                                                                                                                                                                                                                                                                                                                                GTNKTDVVCGFQSRMRTLVVIPVTMGVLFAVLL-----VSACIRNITKKRQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSSSHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGLVEQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWL-VTKAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEGTLNTDTICVCVEGQHC---TSHTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCPPGTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVRLPLQCLFWGFFLTAVHSEPATACGEKQYPVNSLCCDLCPPGQKLVNDCTEVSKTECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B-cell; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >269
193
215
>269
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%;
28.0%;
                                                                                                                                                                       Last sequence update)
Last annotation update)
SOLUBLE RECEPTOR PRECURSOR
                                                                                                                                                                                                                                           Created)
                                                                                                            on
                                                                                                          n Kasza)
RNA stag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 267; DB 1
Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                          stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746903F30F95F387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                              (SFV)
                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. . .)
                                                                                                            Poxviridae;
                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                           (PROTEIN
                                                                                                          Chordopoxvirinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 6
TNR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M17433; -; NOT_ANNOTATED_CDS.
EMBL; A23727; CAA01687.1; -.
PIR; B43692; B43692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91207415; PubMed=1850261;
Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Upton C., Delange A.M., McFadden G.; "Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome."; Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00020; TNFR_c6; 2. ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00208; TNFR; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19438; 1TNR
                                                                                   177
                                                                                                                         180
                                                                                                                                                               118
                                                                                                                                                                                                       133
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                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                    20 VLRLVLYLTFLGAPCYAPALP-----SCKEDEYPVGSECCPKCSPGYRVKEACGELTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIVIRAL EFFECTS OF THE CYTOKINE.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chem. Biophys. Res. Commun. 176:335-342(1991) FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBAR REACH CELLULAR TARGET AND THEREBY DEAMPENING
                                                                                 LYPVNETSCT---TTAG
                                                                                                                                                               NGCRIC-APQTKCPAGYGVSGHTRAGDTLCEKCPPHTYSDSLSPTERCGTSFNYISVGFN
                                                                                                                                                                                                       DHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEEC------
                                                                                                                                                                                                                                                                                       VCEPCPPGTYTAHLNGLSKCLQCQMCDPAMG-LRASRNCSRTENAVCGCSPGH;CIVQDG
                                                                                                                                                                                                                                                                                                                               MLRLIALLVCV-VYVYGDDVPYSSNQGKCGGHDYEKDGLCCASCHPGFYASRLCGPGSNT
                                                                                                                       ---QHQTKCSWLVTKAG
                                                                                                                                                                                                                                               VCSPCEDGTFTASTNHAPACVSCR--GPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00652; TNFR_NGFR_1; 2.
PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001368; TNFR_c6
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                                                                                                                                                                                                                                                                                                                                                                                                                               16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Commun. 176:335-342(1991).
THE ALPHA AND BETA. PROBABLY PREVENTS
                                                                                   190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
4 X TWNR-CYS.
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 260;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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P20333;
01-FEB-1991
01-AUG-1991
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECROSIS FACTOR
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT)
TNFRSFIB OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96299745; pubMed=8661109;
Beltinger C.P., White P.S., Maris J.M.,
Lepaslier D., Stallard B.J., Goeddel D.
Brodeur G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99221490;
Park Y.C., Burkit
                                                  Characterization of ligand phosphorylation.";
                                                                             MEDLINE=93016040; PubMed=1328224; Pennica D., Lam V.T., Mize N.K., 1 Lipari M.T., Goeddel D.V.;
                                                                                                   CHARACTERIZATION. MEDLINE=93016040;
                                                                                                                                           distinct
                                                                                                                                                                                  MEDLINE-91056048;
                                                                                                                                                                                             SEQUENCE OF 23-40;
                                                                                                                                                                                                              "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";

"J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                         Engelmann H., Novick D., Wallach
                                                                                                                                                                                                                                                                                                           "Complementary and demonstrati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A receptor for tumor necrosis factor cellular and viral proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                     X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                  MEDLINE=90110215; PubMed=2153136;
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                               Loetscher H.,
Brockhaus M.;
                                                                                                                                                                                                                                                                                                                                          Heller R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90260639;
                                                                   "Biochemical properties of the 75-kDa
                                                                                                                                                                                                                                                                                                                                                                                            "Physical
                                                                                                                                          Purification and partial amino acid sequence analysis of two listinct tumor necrosis factor receptors from HL60 cells.";
                                         Biol.
                                                                                                                                                                                                                                                                                                           demonstration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              =90260639; PubMed=2160731;
.A., Davis T., Anderson D.,
.K., Cosman D., Goodwin R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r and viral proteins.";
248:1019-1023(1990).
                                                                                                                                                                                                                                                                              OF
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                                                                                                                                                                                                                                                                                                 Acad.
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                                                                                                                                necrosis factor receptors
265:20131-20138(1990).
                                                                                                                                                                                                                                                                                               DNA cloning of a receptor for tumor necrosis ion of a shed form of the receptor."; ad. Sci. U.S.A. 87:6151-6155(1990).
                                        267:21172-21178(1992).
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; PubMed=2166946;
g K., Onasch M.A.,
PubMed=10206649;
t V., Villa A.R.,
                                                                                                                                                                                  PubMed=2173696;
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Phosphorylation;
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modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural basis
human TRAF2.";
                                                                                                                                                                                     PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF TWER2 LINKED TO AN IMMUGLOBULIN EC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
WWW-"http://www.enbrelinfo.com/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR FOR THE ALPHA, HIGH AFFILITY F APPROXIMATELY 5-FOLD LOWER AFFILITY FOR THE-BETA. SUBCELLULAR LOCAFION: TYPE I MEMBRANE PROTEIN. PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WI
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equires a license agreement (Semail to license@isb-sib.ch).
                                                                                             Bioinformatics Institute.
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                      http://www.isb-sib.ch/announce/
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M35857; AAA63262.1.

W52165; AAC50622.1.

W52157; AAC50622.1.

W52158; AAC50622.1.

W52159; AAC50622.1.

W52159; AAC50622.1.

W52161; AAC50622.1.

W52161; AAC50622.1.

W52162; AAC50622.1.

W52163; AAC50622.1.

W52164; AAC50622.1. AAA59929. AAA63262. JOINED.

mbrane; Glycoprotein;
Pharmaceutical; 3D-st; TNFR\_NGFR\_2; 4.

3D-structure NECROSIS

Repeat;

Signal;

461 257 287 287 201 201 118 118 118 201 53 75 201 118 118 110 110 1118

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CYTOPLASMIC TUMOR NECROSIS

TNFR-CYS

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Best Local :
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PIR; S35987; S35987.
PIR; S46888; S46888.
HSSP; P19438; INCF.
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SEQUENCE
                                                                                                                   InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-INDIA-1967 / ISOLATE IND3;

MEDLINE-93202281; PubMed-8384129;

Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;

"Genes of variola and vaccinia viruses necessary to protective mechanisms.";

EFBG Tett 710-80-70-70-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P34015;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PROTEIN C22/B28 HOMOLOG.
                                                                                                                                                                                                                                                                                                                 EMBL; X69198; CAA49137.1; -. EMBL; X67117; CAA47540.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S LETT. 319:80-83(1993).
SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
R -> P (IN REF. 4).
R -> M (IN REF. 1 AND 3).
R -> T (IN REF. 4).
MW; 603B580ECD67636F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 259; DB
Pred. No. 7.5e
23; Mismatches
2 X TNFR-CYS.
TNFR-CYS 1.
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                                                                           NN
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.5e-14;
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RESULT
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Best Local
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                                     EMBL; L04270;
HSSP; P25942;
MIM; 600979; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p36941;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
SEQUENCE
                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                           This
                                                                                                                                                                                                                                                            Crowe P.D., van Arsdale T.L., Walter B.N., Ware Ehrenfels B., Browning J.L., Din W.S., Goodwin "A lymphotoxin-beta-specific receptor."; Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                          Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
          InterPro; IPR0
Pfam; PF00020;
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
MEDLINE=93252381; PubMed=8486360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTBR OR TNFCR OR TNFRSF3. Homo sapiens (Human).
                                                                                                                                              the European Bioinformatics Institute.

    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION

                                                                                                                                                                                                                                                                                                                   MEDLINE=94225209; PubMed=8171323;
                                                                                                                                                                                                                                                                                                                                    FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNRC_HUMAN
                                                                                                                                                                                                                                               -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LRLVLYLTFLGAPC------YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL
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                                                                                                                                                                                                                                    IMMUNE
                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YIDVEITLYPVNDTSCTRTTT---TGLSES----ILTSELTITM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKSVLYLYILFLSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECQ------HQTKCSWLVTKAGAGTSSSHWVWWFLSGSLVIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGSSGCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFN
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          IPR001368; TNFR_
0020; TNFR_c6; 4
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                                                   1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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29.3%;
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D45D40B5C6E780EF
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Catarrhini;
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No. 8.4e-14;
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                                                                                                                                 There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Å
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dwin R.G., S
                                                                                                       . Usage by and for http://www.isb-sib.cl
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Smith C./
                                                                                                                                                restrictions on
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L outstation -
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RESULT
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Best Local S
Matches 86
                                                    U1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
LIBR OR INFECR.
                                                                                                         TNRC_MOUSE
P50284;
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DOMAIN
REPEAT
SEQUENCE FROM N.A
               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                     YFPDL----VQPLLPISGDVSP
                                                                                                                                                                                       --PDVTTVAVEETIPSFTGRSP
                                                                                                                                                                                                                             VIVCSTVGLII-----CVKRRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAP----
                                                                                                                                                                                                                                                 KAGHFQNTSSPSA---RCQPHTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTMLM
                                                                                                                    MOUSE
                                                                                                                                                                                                            LAVLLPLAFFLLLATVFSCIWKSHP--SLCRKLGSLLKRRPQGEGPNPVAGSWEPPKAHP
                                                                                                                                                                                                                                                                                         TSKRKTQCRCQPGMFCAAW-ALECTHCELLSDCPPGTEAELKDEVGKGNNH----
                                                                                                                                                                                                                                                                                                            SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPG-----QRVQKGGTESQDTLCQNC
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42
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                                               (Mouse)
                                                                                                                                                                                                                                                                   SPNGTLEECQHQTKC-SWLVTKAGAGTSSSHWVWW-----FLSGSLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                    STANDARD;
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TNFR_NGFR_2; 3.
                           Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%;
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                              37; Mismatches
                                                                                                                                                                     303
                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 253; DB 1;
Pred. No. 2.2e-13;
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYMPHOTOXIN-BETA RECEPTOR EXTRACELLULAR (POTENTIAL)
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                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .) (P-LINKED (GLCNAC. . .) (P-LINKED (GLCNAC. . .) (P624626E6022F656F CRC64;
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뫄 Qy

14

WGP---

-PPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEY--

CWD---

ODKEYYE

52 47 83; Conservative

40;

83;

Gaps

15;

WGPLLLGLSGLLVASQPQLVPPYRIENQT - -

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STATES TO THE TREE TO THE TENT OF THE TENT
Query Match
Best Local S
Matches 83
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                                                                                                                                                                              REPEAT
DISULFID
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SEQUENCE
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TRANSMEM
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SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence trap and chromosomal mapping Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96163885;
Nakamura T., Tash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U29173; AAA68964.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honjo T.;
The murine lymphotoxin-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CVB; TISSUE=Lung;
MEDLINE=96072804; PubMed=7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse lymphotoxin-beta receptor.
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U30798; AAA81334.1;
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P15725;
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                                                                                                                                                                                                                                                                              ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001368; INFR_c6.
Pfam; PF00020; INFR_c6; 3.
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PIR; S12783; S12783.
HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive."
Tymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
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Rattus norvegicus (Rat).
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01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
0X40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
SUBCELLULAR LOCATION: TYPE I MEMBRAME PROTEIN.
TISSUE SPECIFICITY: ACTIVATED T-CELLS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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requires a license agreement (See
an email to license@isb-sib.ch).
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TNFR_NGFR_2; 2.
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                                                                                                                                                                                                       Glycoprotein; Transmembrane; Repeat;
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                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                            OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
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                                          TNFR-CYS
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P29825;
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CARBOHYD
                                                              PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; Glycoprotein; Repeat; Signal.
                                                                                                                              Pfam; PF00020; TNFR_c6; 2. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                        EMBL; M95181; AAA46632.1; -. EMBL; A23729; CAA01688.1; -. PIR; A40566; GQVZML.
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extremena Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Upton C., Macen J.L., Schreiber M., McFadden G.; "Myxoma virus expresses a secreted protein with homology necrosis factor receptor gene family that contributes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR
                                                                                                                                                                                                 InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                      HSSP; P19438;
                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 184:370-382(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myxoma virus (strain Lausanne)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIVIRAL EFFECTS OF THE CYTOKINE.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REACH CELLULAR TARGET AND THEREBY DEAMPENING
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51; Conser
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TNER-CYS 2.
TNER-CYS 3 (INCOMPLETE).
TNER-CYS 4.
N-LINKED (GLOWN
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POTENTIAL.
TUMOR NECROSIS
4 X INFR-CYS.
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Pred. No. 1.4e-12;
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                       FACTOR
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Best Local
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077736;
15-JUL-1999 (Rel. 38, C
15-JUL-1999 (Rel. 38, I
20-AUG-2001 (Rel. 40, I
                                                                                    myocardium of pig.",

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                   FASL RECEPTOR PRECURSOR (APO-1 ANTIGEN) (CD95).
TNFRSF6 OR APT1 OR FAS.
Sus scrofa (Pig).
             This
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammaila; Eutheria; Cetartiodactyla; Suina; Suidae;
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REPEAT
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                                                                                                                                                                                                                                                         Bartling
                                                                                                                                                                                                                                                                        SEQUENCE FROM
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Expression of apoptosis-associated
Bartling of pig ".
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                                     SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                               DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                         UL-1999 (Rel. 38, Last sequence update)
UG-2001 (Rel. 40, Last annotation update)
RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRYQNTTKMCTLNIEIRCVE----GDAVRTI 260
SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----HQTKCSWLVTKAGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LVIVIVCSTVGLIICVKRRKPRGDVVKVI
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P47741;
01-FEB-1996 (Rel. 33, 0
01-FEB-1996 (Rel. 33, 1
20-AUG-2001 (Rel. 40, 1
                                                                                                               20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 0X401 RECEPTOR PRECURSOR (OX40 ANTIGEN). TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                   MOUSE
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CARBOHYD
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MEDLINE=94044750; PubMed=8228223; Calderhead D.M., Buhlmann J.E., v Calderhead E., Noelle R.J., Fell H. Claassen E., Noelle R.J., Fell H. "Cloning of mouse Ox40: a T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
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SMART; SM00208; TNFR; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                           SEQUENCE FROM STRAIN-BALB/C;
                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                           NCBI_TaxID=10090;
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Rodentia;
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TNFR-CYS 2.
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P25119; P97893;
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SIGNAL
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Eur. J. Immunol. 25:926-930(1995).
-i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birkeland M.L., Barclay A.N.;
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Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.
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[mmunol. 151:5261-5271(1993).
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X85214;
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PS50050; TMFR_NGFR_2; 2.
PS50050; TMFR_NGFR_2; 2.
  (Rel. 22, Created)
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EMBL; M59378; AAA40463.1; -
EMBL; M59378; CAA65021.1; -
EMBL; X87128; CAA60618.1; -
PIR; B38634; B38634.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                 ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
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Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacob C.O., Liu J.;
Submitted (JAN-1996) to the
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                                                                                                                                                                                                      Receptor;
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                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                   TNFR_NGFR_1;
TNFR_NGFR_2;
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Rodentia;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91246168; PubMed=1645445;
Goodwin R.G., Anderson D., Jerzy R., Dav
Copeland N.G., Jenkins N.A., Smith C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: RECEPTOR FOR TWF-ALPHA.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TWFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor receptors demonstrate
specific.";
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TNFR-CYS 4...
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EMBL/GenBank/DDBJ
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                                                                                                                            TNFR-CYS
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                                                                                                                                                                                                            4 X TNFR-CYS
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                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                            Biochem. Biophys. Res. Commun. 198:666-674(1994).

-:- FUNCTION: RECEPTOR FOR A CYTOKINE LICAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASSPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTANE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-WEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
(APO-1 ANTIGEN) (CD95).
TNFRSF6 OR PT1 OR FAS.
                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver; MEDLINE-94128114; PubMed-7507668; Kimura K., Yamamoto M., Wakatsuki T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant mRNA species encoding a truncated form
  European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat liver.";
                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Sciurognathi; Muridae;
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Pfam; PF00020; TNFR_C6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS50059; TNFR_NGFR_2; 2.

PROSITE; PS50017; DEATH_DOMAIN; 1
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                                                                                                                                                                                                                                   CDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQ 158
                                                                                                                                                                                                                                                                                  NCSEGLYQVGPFCCQPCQPGERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAF 102
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58; Conser
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Pred. No. 9.1e-10;
7; Mismatches 93
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3 X TNFR-CYS.
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Search completed: January 24, 2002, 16:25:16 Job time: 191 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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sp_rodent:*
sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result (	1 1303.5	2 271.5	3 269.5	4 269.5	5 269.5	6 269.5	7 269.5	268	9 268.5	_			265	N	15 262.5	ь)		N	17 259 18 257.5
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Query Match Length	283	349	348	348	349	. 349	349	222	234	349	. 349	348	349	260	349	169	349	348	
DB	6	12	12	12	12	12	12	11	11	12	12	12	12	11	12	11	12	12	د
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otion	cercopithec			~	. monkeypox	monkeypox	monkeypox	l mus musculu		camelpox v	-		_		-	_	•	variola	-

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Query Match 82.6 Best Local Similarity 82.0 Matches 232; Conservative

82.6%; Score 1303.5; DB 6; Length 283:. 82.0%; Pred. No. 4.4e-116; Live 18; Mismatches 30; Indels 3;

Gaps

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		43																				23	22	21	
218	219.5	219.5	225.5	225.5	226.5	227	228	228	228.5	229	229.5	232.5	236.5	239	243.5	246	249	249.5	251.5	254.5	254.5	257	257	257	257.5
13.8	13.9	13.9	14.3	14.3	14.4	14.4	14.4	14.4	14.5	14.5	14.5	14.7	15.0	15.1	15.4		15.8						16.3		
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Q9XS29	Q9TV79	002764	Q85308	057115	057123	Q9DGH7	057118	Q9DGH8	057120	057119	057122	057305	057121	057116	073559	095407	057109	Q9BYU0	Q99NE3	Q9DFV0	Q16042	289098	Q89118	057110	057117
Q9xs29 oryctolagus	Q9tv79 oryctolagus	002764 oryctolagus	Q85308 cowpox viru	057115 cowpox viru	cowpox	gallus				cowpox		O57305 cowpox viru	O57121 cowpox viru	O57116 cowpox viru	073559 cowpox viru	095407 homo sapien	O57109 variola vir	Q9byu0 homo sapien	Q99ne3 mus musculu	Q9dfv0 brachydanio	Q16042 homo sapien		Q89118 variola vir	057110 variola vir	O57117 cowpox viru

## ALIGNMENTS

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Pfam; PF00020; TNFR_C6; 3.  ProDom; PD000771; TNFR_C6; 1.  SMART; SM00208; TNFR; 3.  PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.  PROSITE; PS50050; TNFR_NGFR_2; 2.  PROSITE; PS50050; TNFR_NGFR_2; 2.  SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;	green iluorescence protein."; Virology 258:365-374(1999). EMBL; AF147720; AAD37381.1; HSSP; P25942; ICDF.	MEDIINE-9296730; PubMed=10366573; MEDIINE-9296730; PubMed=10366573; Foster T.P., Chouljenko V.N., Kousoulas K.G.; Functional characterization of the HveA homolog specified by African green monkey kidney cells with a herpes simplex virus expressing the	copithecus	HYEAS. HYEAS. HYEAS. Cercopithecus aethiops (Green monkey) (Grivet). Cercopithecus aethiops (Green monkey) (Grivet). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;	03XSZ8; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	LT 1 Z8 Q9XSZ8 PRELIMINARY; PRT; 283 AA.

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RESULT
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ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2
PROSITE; PS50050; TNFR_NGFR_2; 2
SEQUENCE 349 AA; 38239 MW; D
                057277;
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01-JUN-1998
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Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U87844; AAB94361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, Orthopoxvirus.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                     Last sequence update)
                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 271.5; DB 12; Length Pred. No. 7.6e-18; Indels
                                                                                                 PRT;
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2.
DF6C280D478F2422 CRC64;
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 $\sum_{\mathbf{k},j}$ 

Query Match 17.1%; S Best Local Similarity 32.6%; P Matches 57; Conservative 25;

Score 269.5; DB 12 Pred. No. 1.2e-17; 5; Mismatches 78;

DB 12;

Indels Length 348;

15;

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Best Local Similarity
Matches 57; Conserv
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
SEQUENCE 348 AA; 38212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001338; TNFR_C6.
Pfam; PF00020; TNFR_C6; 2.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00052; TNFR_NGFR_1; 2
PROSITE; PS50050; TNFR_NGFR_2; 2
SEQUENCE 348 AA; 38212 MW; 5.
                                                                                                                                                                                                                                                                                       057108; PRELIMINARY; PRT; 348 AA. 057108; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLE). 17, Last annotation update)
                                                                                                                                   Loparev V.N., Parsons J.M., Submitted (FEB-1997) to the
                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ZAIRE-1970 (CONGO-8);
                                                                                                                                                                                                                                                                     CRMB.
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LOPATEV V.N., PATSONS J.M., ESPOSITO J.J.;
SUDMITTED (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; U88543; AAB94378.1; -.
EMBL; U87841; AAB94358.1; -.
HSSP; P25942; 1CDF.
                                                                                                     EMBL; U88142; AAB94367.1; -. HSSP; P25942; 1CDF.
                                                                                                                                                                                                                        Orthopoxvirus:
                                                                                                                                                                                                                                    Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                      Monkeypox virus
                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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                                                                                                                                                                                                         NCBI_TaxID=10244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRSVLYSYILFLSCIIINGRDLAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK 60
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  ; TNFR_NGFR_1; 2.
; TNFR_NGFR_2; 2.
A; 38212 MW; E5!
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32.6%;
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                                                                                                                                   Esposito J.J.;
EMBL/GenBank/DDBJ
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2.
E555979057DEC91F CRC64;
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2.
54019521556C2D8F CRC64;
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Best Local S
Matches 59
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Submitted (JAN-1998) to the EM
EMBL; U88144; AAB94369.1; -
EMBL; U87842; AAB94359.1; -
EMBL; U87994; AAB94365.1; -
EMBL; U87995; AAB94366.1; -
EMBL; U88143; AAB94368.1; -
EMBL; U88143; AAB94368.1; -
057101
057101;
01-JUN-1998
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Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
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STRAIN=VARIOUS STRAINS;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                            MRSVLYSYTLFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK
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                                                                                                                                                                                                                                    QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLV 189
                                                                                                                                                                                                                                                                                                         TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
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                                                                                                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                   59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00652; TNFR_NGFR_1;
PS50050; TNFR_NGFR_2;
349 AA; 38295 MW;
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   (TremBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rEMBLrel. 06, Last sequence update) rEMBLrel. 17, Last annotation update) FACTOR RECEPTOR II HOMOLOG.
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17,
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   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 269.5; DB 1
Pred. No. 1.2e-17;
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                                     PRT;
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2.
CBD2C949ED2B8E7C CRC64;
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Best Local Similarity
Matches 59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                057102
057102;
                                                                                                                                                                                                                                                                 Orthopoxvirus.
NCBI_TaxID=10244;
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InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 2.

Pr0Dom; DP000071; TNFR_c6; 1.

SMART; SM00208; TNFR; 2.

PR0SITE; PS00652; TNFR_NGFR_1; 2

PR0SITE; PS50050; TNFR_NGFR_2; 2

SEQUENCE 349 AA; 38308 MW; C
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Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U87845; AAB94362.1; -.
HSSP; P25942; 1CDF.
InterPro; IPR001358; TNFR_C6.
Pfam; PF00020; TNFR_C6; 1.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BENIN-1978 (78-3945);
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                         EMBL; U87846; AAB94363.1; HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYS-----HTVSSTDKCEPVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNTQCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCLL 118
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32.6%;
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                                                                                                                                                                                                                                                                                                                                                                                               RNA stage; Poxviridae; Chordopoxvirinae;
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Pred. No. 1.2e
22; Mismatches
  2;
2;
CBD2C949F994C59C CRC64;
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02F65B00CFB858BE CRC64;
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Matches 59
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Best Local
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       Q99NE2;
Q99NE2;
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                 MEDLINE=21117110; pubMed=11172023;
Tone M., Tone Y., Fairchild P.J., Wykes M., Wald "Regulation of CD40 function by its isoforms gen aiternative spilicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001)
EMBL; AJ401389; CAC29499 MW; EE21E6C76FB42DEF
                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CD40 TYPE IV ISOFORM.
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                                                                                                                                 LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
                                                                                                                                                  PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT
                                                                                                                                                                   PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                    {\tt TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE}
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59; Conser
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32.6%;
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Pred. No. 1.2e
22; Mismatches
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Pred. No. 9e
                                  PRT;
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Best Local
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                                                                                                                                                                                            NCBI_TaxID=28873;
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               l Similarity
57; Conserv
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               16.9%; ilarity 33.1%; Conservative 2.
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STRAIN-DUBAL 1992 (CP-5), SOMALIA-1978;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ dat
EMBL; U87840; AAB94357.1; -.
EMBL; U87837; AAB94357.1; -.
EMBL; U87837; AAB94354.1; -.
HSSP; P25942; ICDE
InterPro; IPRO1156; TNFR_C6.
Pfam; PF00020; TNFR_C6; 2.
PF0D0m; PD000771; TNFR_C6; 1.
SARRT; SM00208; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_2; 2.
SEQUENCE 349 AA; 38036 MW; EA412AEE86E090E4 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             057284 PRELIMINARY; PRT; 349 AA. 057284; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Camelpox virus (strain (Viruses, dsDNA viruses, Orthopoxvirus
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MEDITINE=21117110; PubMed=11172023;

Tone M., Tone Y., Fairchild P.J., Wykes M., Waldm
Tone M., Tone Y., Fairchild P.J., Wykes M., Waldm
"Regulation of CD40 function by its isoforms gene
aiternative spilicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

EMBL; AJ401388; CAC2948.1; - CODBIRD 29147F375 C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK---GTSQTNVICGLKSRMRALLVI 198
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Score 266.5;
Pred. No. 2.3e
24; Mismatches
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Pred. No. 9.5e-18;
                                                                                                                          2.
2.
EA412AEE86E090E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poxviridae; Chordopoxvirinae;
                          3e-17;
                                                 DB 12;
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RESULT 057103 ID 057103 PM 05 
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Best Local
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Loparev V.N., Parsons J.M., Esp
Submitted (JAN-1997) to the EMI
EMBL; U87839; AAB94356.1; -.
HSSP; P25942; 1CDF.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                   O57103 PRELIMINARY; PRT; 348 AA. 057103; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                               Orthopoxvirus
                                                                                                                                                                    Monkeypox virus
                                                                                                                                                                                                                  CRMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00020; TNFR_C6; 2. ProDom; PD000771; TNFR_C6; 1. SMART; SM00208; TNFR; 2.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       057098;
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                                              NCBI_TaxID=10244;
                                                                                                                                  Viruses;
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33.1%;
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Pred. No. 2.3e-17
24; Mismatches 70
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EMBL/GenBank/DDBJ databases.
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Matches 56; Conserv
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057099;
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Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U87847; AAB94364.1; -
HSSP; P25942; 1CDF.
InterPro; IPR001368; TMFR_C6.
Pfam; PF00020; TMFR_C6; 2.
ProDom; PD000771; TMFR_C6; 1.
SMART; SM00208; TMFR; 2.
                                                                                                                                                                                                                                                                                          STRAIN-SIERRA LEONE-1970 (70-0266);
Loparev V.N., Parsons J.M., Espositu
Submitted (JAN-1997) to the EMBL/Gen
EMBL; U87843; AAB94360.1; -.
HSSP; P25942; 1CDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG
                                                                                                                                                                                       PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; SEQUENCE 349 AA; 38321 MW;
                                                                                                                                                                                                                                  Interpro: IPR001368; TNFR_c6.
pfam; pr00020; TNFR_c6; 2.
proDom; pD000077; TNFR_c6; 1.
smart; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                               Orthopoxvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Monkeypox virus.
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LRLVLYLTFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
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                                                                        LRLVLYITFLGAPC-----YAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGEL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQHQT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
TNTQCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCLL
                            TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                           MRSVLYSYILFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNTQCTPCGSDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRSALYSYILFLSCIIINGRDIAPHAPSNGKCKDNEYRSRNLCCLSCPPGTYASRLCDSK 60
                                                                                                                   Similarity
59; Conser
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                               16.8%;
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32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           RNA stage;
                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                      Esposíto
                                                                                                                Score 265.5; DB 12;
Pred. No. 2.8e-17;
2; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 265.5; DB 1
Pred. No. 2.8e-17;
                                                                                                                                                                                 2.
FE449028CC933F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.
34A5E668B27907B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                      J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                                                                                                                                           Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                             DB 12;
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                                                                                                                   Indels
                                                                                                                                             Length 349;
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                                                                                                                   19;
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Best Local S
Matches 68
EMBL;
         SEQUENCE FROM N.A.
STRAIN-IRAN (DP-1);
LOPATEV V.N., PATSONS J.M.,
Submitted (JAN-1997) to the
EMBL; U87838; AAB94355.1; -.
                                                                                                                                                           057097 PRELIMINARY: PRT; 349 AA. 057097; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
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MEDLINE-2111710; PubMed=11172023;

MEDLINE-21117110; PubMed=11172023;

Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.

"Regulation of CD40 function by its isoforms generated alternative spilicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

EMBL; AJ401390; CAC29430.1; -.

SEQUENCE 260 AA; 28895 MW; 57A5BACE8CF2F546 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD40.

CD40.

Mus musculus (Mouse).

Mus musculus (Mouse).

Metazoa; Chordata;

Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99NEO;
                                                                                                         Orthopoxvirus
                                                                                                                   Camelpox virus (strain CP-1).
Viruses; dsDNA viruses, no RN
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CD40 TYPE V ISOFORM.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                           NCBI_TaxID=28873;
                                                                                                                                                                                                                                                                                                     184
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                                                                                                                                                                                                                                                                                                                                                                        LCQNCPPGTFSPNGTL-EECQHQTKCS----WLVTKAGAGTSSSHWVWWFLSGSLVIVIV 215
:| || || || :|
                                                                                                                                                                                                                                                                                                                                                       VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQK----GTSQTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                  PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCKEDEYPYGSECCPKCSPGYRYKEACGELTGTYCEPCPPGTYIAHLNGLSKCLQCQMCD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 173
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                                                                                                                                                                                                                                                                                                                            CSTVGLIICVK-RRKPRGDVVKVIVSVQRKRQEAEGEATVIEALQAPPDVTTVAVEETI 273
                                                                                                                                                                                                                                                                                                                                                                                                              PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD---CEACAQHTPCIPGFGVMEMATETTDT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGALGCRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYS-----HTVSSTDKCEPVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                    ----VICEKVVKKPKDN--EMLPPAARRQDPQEME------DYPGHNTAAPVQETL
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17,
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                                                                                                                       RNA stage;
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Last sequence update)
Last annotation update)
                        Exposito J.J.;
EMBL/GenBank/DDBJ databases
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Pred. No. 2.3e-17;
4; Mismatches 95;
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                                                                                                                      Poxviridae; Chordopoxvirinae;
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Best Local Similarity
Matches 57; Conserv
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Pfam; PF00020; TNFR_c6; 2.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 3

PROSITE; PS500652; TNFR_NGFR_1; 1

PROSITE; PS500650; TNFR_NGFR_2; 2

SEQUENCE 349 AA; 37944 MW; 8
                                                                                                                                                                                                                                                                                                                       HSSP; P25942; 1CDF
 119
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                                                                             71
                                                                                                                      TGTVCEPCPPGTYIAHLNGLSKCLQCQ-MCDPAMGLRASRNCSRTENAVCGCSPGHFCIV 129
                                                                                                        MKSVLYSYILFLSCIIINGRDVTPYAPSNGKCKDNEYKRHNLCCLSCPPGTYASRLCDSK 60
KGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSRTVSSADKCE
                        QDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFSPN-GTLEECQ 180
                                                    TNTQCTPCGSGTLTSRNNHLPACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCIL
                                                                                                                                                             Conservative
                                                                                                                                                                        16.6%;
                                                                                                                                                          23;
                                                                                                                                                         Score 262.5;
Pred. No. 5.4e
23; Mismatches
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2.
829EA54ED4C60455 CRC64;
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77;
                                                                                                                                                           Indels
                                                                                                                                                                                    Length 349;
169
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